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(54) Title: HLA-BINDING PEPTIDES AND THEIR USES

(57) Abstract

The present invention provides the means and methods for selecting immunogenic peptides and the immunogenic peptide compositions capable of specifically binding glycoproteins encoded by HLA allele and inducing T cell activation in T cells restricted by the allele. The peptides are useful to elicit an immune response against a desired antigen.

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HLA BINDING PEPTIDES AND THEIR USES

BACKGROUND OF THE INVENTION

The present invention relates to compositions and methods for preventing, treating or diagnosing a number of pathological states such as viral diseases and cancers.

5 In particular, it provides novel peptides capable of binding selected major histocompatibility complex (MHC) molecules and inducing an immune response.

MHC molecules are classified as either Class I or Class II molecules. Class II MHC molecules are expressed primarily on cells involved in initiating and sustaining immune responses, such as T lymphocytes, B lymphocytes, macrophages, etc. Class II 10 MHC molecules are recognized by helper T lymphocytes and induce proliferation of helper T lymphocytes and amplification of the immune response to the particular immunogenic peptide that is displayed. Class I MHC molecules are expressed on almost all nucleated cells and are recognized by cytotoxic T lymphocytes (CTLs), which then 15 destroy the antigen-bearing cells. CTLs are particularly important in tumor rejection and in fighting viral infections.

The CTL recognizes the antigen in the form of a peptide fragment bound to the MHC class I molecules rather than the intact foreign antigen itself. The antigen must normally be endogenously synthesized by the cell, and a portion of the protein antigen is degraded into small peptide fragments in the cytoplasm. Some of these small peptides 20 translocate into a pre-Golgi compartment and interact with class I heavy chains to facilitate proper folding and association with the subunit β 2 microglobulin. The peptide-MHC class I complex is then routed to the cell surface for expression and potential recognition by specific CTLs.

Investigations of the crystal structure of the human MHC class I molecule, 25 HLA-A2.1, indicate that a peptide binding groove is created by the folding of the α 1 and α 2 domains of the class I heavy chain (Bjorkman et al., *Nature* 329:506 (1987)). In these investigations, however, the identity of peptides bound to the groove was not determined.

Buus et al., *Science* 242:1065 (1988) first described a method for acid elution of bound peptides from MHC. Subsequently, Rammensee and his coworkers (Falk

et al., Nature 351:290 (1991) have developed an approach to characterize naturally processed peptides bound to class I molecules. Other investigators have successfully achieved direct amino acid sequencing of the more abundant peptides in various HPLC fractions by conventional automated sequencing of peptides eluted from class I molecules of the B type (Jardetzky, et al., Nature 353:326 (1991) and of the A2.1 type by mass spectrometry (Hunt, et al., Science 225:1261 (1992). A review of the characterization of naturally processed peptides in MHC Class I has been presented by Rötzschke and Falk (Rötzschke and Falk, Immunol. Today 12:447 (1991).

Sette et al., Proc. Natl. Acad. Sci. USA 86:3296 (1989) showed that MHC allele specific motifs could be used to predict MHC binding capacity. Schaeffer et al., Proc. Natl. Acad. Sci. USA 86:4649 (1989) showed that MHC binding was related to immunogenicity. Several authors (De Bruijn et al., Eur. J. Immunol., 21:2963-2970 (1991); Palmer et al., 991 Nature 353:852-955 (1991)) have provided preliminary evidence that class I binding motifs can be applied to the identification of potential immunogenic peptides in animal models. Class I motifs specific for a number of human alleles of a given class I isotype have yet to be described. It is desirable that the combined frequencies of these different alleles should be high enough to cover a large fraction or perhaps the majority of the human outbred population.

Despite the developments in the art, the prior art has yet to provide a useful human peptide-based vaccine or therapeutic agent based on this work. The present invention provides these and other advantages.

SUMMARY OF THE INVENTION

The present invention provides compositions comprising immunogenic peptides having binding motifs for HLA molecules. The immunogenic peptides, which bind to the appropriate MHC allele, comprise conserved residues at certain positions which allow the peptides to bind desired HLA molecules.

Epitopes on a number of immunogenic target proteins can be identified using the peptides of the invention. Examples of suitable antigens include prostate cancer specific antigen (PSA), hepatitis B core and surface antigens (HBVc, HBVs) hepatitis C antigens, Epstein-Barr virus antigens, human immunodeficiency type-1 virus (HIV1), Kaposi's sarcoma herpes virus (KSHV), human papilloma virus (HPV) antigens, Lassa

virus, mycobacterium tuberculosis (MT), p53, CEA, trypanosome surface antigen (TSA) and Her2/neu. The peptides are thus useful in pharmaceutical compositions for both therapeutic and diagnostic applications.

5 In particular, the invention provides compositions comprising an immunogenic peptide having an HLA binding motif, which immunogenic peptide is a peptide shown in Tables 3-14. Also provided are peptides comprising a conservative substitution of a residue in a peptide shown in Table 3-14. The immunogenic peptide of the invention can be further linked to a second oligopeptide. In some embodiments, the second oligopeptide is a peptide that induces a helper T response.

10 The invention further provides nucleic acid molecules encoding immunogenic peptides as shown in Tables 3-14, or peptides comprising a conservative substitution of a residue of a peptide shown in Table 3-14. The nucleic acid may further comprise a sequence encoding a second immunogenic peptide or peptide that induces a helper T response.

15 The peptides provided here can be used to induce a cytotoxic T cell response either *in vivo* or *in vitro*. The methods comprise contacting a cytotoxic T cell with a peptide of the invention.

Definitions

20 The term "peptide" is used interchangeably with "oligopeptide" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other typically by peptide bonds between the alpha-amino and carbonyl groups of adjacent amino acids. The oligopeptides of the invention are less than about 15 residues in length and usually consist of between about 8 and about 11 residues, preferably 9 or 10 residues.

25 An "immunogenic peptide" is a peptide which comprises an allele-specific motif such that the peptide will bind an MHC molecule and induce a CTL response. Immunogenic peptides of the invention are capable of binding to an appropriate HLA molecule and inducing a cytotoxic T cell response against the antigen from which the immunogenic peptide is derived.

30 Immunogenic peptides are conveniently identified using the algorithms of the invention. The algorithms are mathematical procedures that produce a score which

enables the selection of immunogenic peptides. Typically one uses the algorithmic score with a "binding threshold" to enable selection of peptides that have a high probability of binding at a certain affinity and will in turn be immunogenic. The algorithm is based upon either the effects on MHC binding of a particular amino acid at a particular position of a peptide or the effects on binding of a particular substitution in a motif containing peptide.

A "conserved residue" is an amino acid which occurs in a significantly higher frequency than would be expected by random distribution at a particular position in a peptide. Typically a conserved residue is one where the MHC structure may provide a contact point with the immunogenic peptide. At least one to three or more, preferably two, conserved residues within a peptide of defined length defines a motif for an immunogenic peptide. These residues are typically in close contact with the peptide binding groove, with their side chains buried in specific pockets of the groove itself. Typically, an immunogenic peptide will comprise up to three conserved residues, more usually two conserved residues.

As used herein, "negative binding residues" are amino acids which if present at certain positions will result in a peptide being a nonbinder or poor binder and in turn fail to be immunogenic i.e. induce a CTL response.

The term "motif" refers to the pattern of residues in a peptide of defined length, usually about 8 to about 11 amino acids, which is recognized by a particular MHC allele. The peptide motifs are typically different for each human MHC allele and differ in the pattern of the highly conserved residues and negative residues.

The binding motif for an allele can be defined with increasing degrees of precision. In one case, all of the conserved residues are present in the correct positions in a peptide and there are no negative residues in positions 1,3 and/or 7.

The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany it as found in its native state. Thus, the peptides of this invention do not contain materials normally associated with their *in situ* environment, e.g., MHC I molecules on antigen presenting cells. Even where a protein has been isolated to a homogenous or dominant band, there are trace contaminants in the range of 5-10% of native protein which co-purify with the desired protein. Isolated peptides of this invention do not contain such endogenous co-purified protein.

The term "residue" refers to an amino acid or amino acid mimetic incorporated in an oligopeptide by an amide bond or amide bond mimetic.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention relates to the determination of allele-specific peptide 5 motifs for human Class I MHC (sometimes referred to as HLA) allele subtypes, in particular, peptide motifs recognized by HLA alleles.

For HLA-A2.1 alleles a peptide of 9 amino acids preferably has the following motif: a first conserved residue at the second position from the N-terminus selected from the group consisting of I, V, A and T and a second conserved residue at the 10 C-terminal position selected from the group consisting of V, L, I, A and M. An alternate motif is one in which the first conserved residue at the second position from the N-terminus selected is from the group consisting of L, M, I, V, A and T and the second conserved residue at the C-terminal position selected from the group consisting of A and M. The amino acid at position 1 is preferably not an amino acid selected from the group 15 consisting of D, and P. The amino acid at position 3 from the N-terminus is not an amino acid selected from the group consisting of D, E, R, K and H. The amino acid at position 6 from the N-terminus is not an amino acid selected from the group consisting of R, K and H. The amino acid at position 7 from the N-terminus is not an amino acid selected from the group consisting of R, K, H, D and E.

20 The HLA-A2.1 binding motif for peptide of 10 residues is as follows: a first conserved residue at the second position from the N-terminus selected from the group consisting of L, M, I, V, A, and T, and a second conserved residue at the C-terminal position selected from the group consisting of V, I, L, A and M. The first and second conserved residues are separated by 7 residues. Preferably, the amino acid at position 1 25 is not an amino acid selected from the group consisting of D, E and P. The N-terminal residue is not an amino acid selected from the group consisting of D and E. The residue at position 4 from the N-terminus is not an amino acid selected from the group consisting of A, K, R and H. The amino acid at position 5 from the N-terminus is not P. The amino acid at position 7 from the N-terminus is not an amino acid selected from the group 30 consisting of R, K and H. The amino acid at position 8 from the N-terminus is not amino acid selected from the group consisting of D, E, R, K and H. The amino acid at position

9 from the N-terminus is not an amino acid selected from the group consisting of R, K and H.

5 The motif for HLA-A3.2 comprises from the N-terminus to C-terminus a first conserved residue of L, M, I, V, S, A, T and F at position 2 and a second conserved residue of K, R or Y at the C-terminal end. Other first conserved residues are C, G or D and alternatively E. Other second conserved residues are H or F. The first and second conserved residues are preferably separated by 6 to 7 residues.

10 The motif for HLA-A1 comprises from the N-terminus to the C-terminus a first conserved residue of T, S or M, a second conserved residue of D or E, and a third conserved residue of Y. Other second conserved residues are A, S or T. The first and second conserved residues are adjacent and are preferably separated from the third conserved residue by 6 to 7 residues. A second motif consists of a first conserved residue of E or D and a second conserved residue of Y where the first and second conserved residues are separated by 5 to 6 residues.

15 The motif for HLA-A11 comprises from the N-terminus to the C-terminus a first conserved residue of T, V, M, L, I, S, A, G, N, C D, or F at position 2 and a C-terminal conserved residue of K, R, Y or H. The first and second conserved residues are preferably separated by 6 or 7 residues.

20 The motif for HLA-A24.1 comprises from the N-terminus to the C-terminus a first conserved residue of Y, F or W at position 2 and a C terminal conserved residue of F, I, W, M or L. The first and second conserved residues are preferably separated by 6 to 7 residues.

25 These motifs are then used to define T cell epitopes from any desired antigen, particularly those associated with human viral diseases, cancers or autoimmune diseases, for which the amino acid sequence of the potential antigen or autoantigen targets is known.

30 Epitopes on a number of potential target proteins can be identified in this manner. Examples of suitable antigens include prostate specific antigen (PSA), hepatitis B core and surface antigens (HBVc, HBVs) hepatitis C antigens, Epstein-Barr virus antigens, melanoma antigens (e.g., MAGE-1), human immunodeficiency virus (HIV) antigens, human papilloma virus (HPV) antigens, Lassa virus, mycobacterium tuberculosis (MT), p53, CEA, trypanosome surface antigen (TSA) and Her2/neu.

Peptides comprising the epitopes from these antigens are synthesized and then tested for their ability to bind to the appropriate MHC molecules in assays using, for example, purified class I molecules and radioiodinated peptides and/or cells expressing empty class I molecules by, for instance, immunofluorescent staining and flow microfluorometry, peptide-dependent class I assembly assays, and inhibition of CTL recognition by peptide competition. Those peptides that bind to the class I molecule are further evaluated for their ability to serve as targets for CTLs derived from infected or immunized individuals, as well as for their capacity to induce primary *in vitro* or *in vivo* CTL responses that can give rise to CTL populations capable of reacting with virally infected target cells or tumor cells as potential therapeutic agents.

The MHC class I antigens are encoded by the HLA-A, B, and C loci. HLA-A and B antigens are expressed at the cell surface at approximately equal densities, whereas the expression of HLA-C is significantly lower (perhaps as much as 10-fold lower). Each of these loci have a number of alleles. The peptide binding motifs of the invention are relatively specific for each allelic subtype.

For peptide-based vaccines, the peptides of the present invention preferably comprise a motif recognized by an MHC I molecule having a wide distribution in the human population. Since the MHC alleles occur at different frequencies within different ethnic groups and races, the choice of target MHC allele may depend upon the target population. Table 1 shows the frequency of various alleles at the HLA-A locus products among different races. For instance, the majority of the Caucasoid population can be covered by peptides which bind to four HLA-A allele subtypes, specifically HLA-A2.1, A1, A3.2, and A24.1. Similarly, the majority of the Asian population is encompassed with the addition of peptides binding to a fifth allele HLA-A11.2.

TABLE 1

<u>A Allele/Subtype</u>	<u>N(69)</u>	<u>A(54)</u>	<u>C(502)</u>
5	A1	10.1(7)	1.8(1)
	A2.1	11.5(8)	37.0(20)
	A2.2	10.1(7)	0
	A2.3	1.4(1)	5.5(3)
	A2.4	-	-
	A2.5	-	-
10	A3.1	1.4(1)	0
	A3.2	5.7(4)	5.5(3)
	A11.1	0	5.5(3)
	A11.2	5.7(4)	31.4(17)
	A11.3	0	3.7(2)
	A23	4.3(3)	-
15	A24	2.9(2)	27.7(15)
	A24.2	-	-
	A24.3	-	-
	A25	1.4(1)	-
	A26.1	4.3(3)	9.2(5)
	A26.2	7.2(5)	-
20	A26V	-	3.7(2)
	A28.1	10.1(7)	-
	A28.2	1.4(1)	-
	A29.1	1.4(1)	-
	A29.2	10.1(7)	1.8(1)
	A30.1	8.6(6)	-
25	A30.2	1.4(1)	-
	A30.3	7.2(5)	-
	A31	4.3(3)	7.4(4)
	A32	2.8(2)	-
	Aw33.1	8.6(6)	-
	Aw33.2	2.8(2)	16.6(9)
30	Aw34.1	1.4(1)	-
	Aw34.2	14.5(10)	-
	Aw36	5.9(4)	-

Table compiled from B. DuPont, Immunobiology of HLA, Vol. I, Histocompatibility Testing 1987, Springer-Verlag, New York 1989.

* N - negroid; A = Asian; C = caucasoid. Numbers in parenthesis represent the number of individuals included in the analysis.

and the carboxyl group to the right (the C-terminus) of each amino acid residue. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three letter or single letter designations. The L-form of an amino acid residue is represented by a capital single letter or a capital first letter of a three-letter symbol, and the D-form for those amino acids having D-forms is represented by a lower case single letter or a lower case three letter symbol. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or G.

The procedures used to identify peptides of the present invention generally follow the methods disclosed in Falk et al., *Nature* 351:290 (1991), which is incorporated herein by reference. Briefly, the methods involve large-scale isolation of MHC class I molecules, typically by immunoprecipitation or affinity chromatography, from the appropriate cell or cell line. Examples of other methods for isolation of the desired MHC molecule equally well known to the artisan include ion exchange chromatography, lectin chromatography, size exclusion, high performance ligand chromatography, and a combination of all of the above techniques.

In the typical case, immunoprecipitation is used to isolate the desired allele. A number of protocols can be used, depending upon the specificity of the antibodies used. For example, allele-specific mAb reagents can be used for the affinity purification of the HLA-A, HLA-B₁, and HLA-C molecules. Several mAb reagents for the isolation of HLA-A molecules are available. The monoclonal BB7.2 is suitable for isolating HLA-A2 molecules. Affinity columns prepared with these mAbs using standard techniques are successfully used to purify the respective HLA-A allele products.

In addition to allele-specific mAbs, broadly reactive anti-HLA-A, B, C mAbs, such as W6/32 and B9.12.1, and one anti-HLA-B, C mAb, B1.23.2, could be used in alternative affinity purification protocols as described in previous applications.

The peptides bound to the peptide binding groove of the isolated MHC molecules are eluted typically using acid treatment. Peptides can also be dissociated from class I molecules by a variety of standard denaturing means, such as heat, pH, detergents, salts, chaotropic agents, or a combination thereof.

Peptide fractions are further separated from the MHC molecules by reversed-phase high performance liquid chromatography (HPLC) and sequenced. Peptides can be separated by a variety of other standard means well known to the artisan, including filtration, ultrafiltration, electrophoresis, size chromatography, precipitation with specific antibodies, ion exchange chromatography, isoelectrofocusing, and the like.

Sequencing of the isolated peptides can be performed according to standard techniques such as Edman degradation (Hunkapiller, M.W., et al., *Methods Enzymol.* 91, 399 [1983]). Other methods suitable for sequencing include mass spectrometry sequencing of individual peptides as previously described (Hunt, et al., *Science* 225:1261 (1992), which is incorporated herein by reference). Amino acid sequencing of bulk heterogenous peptides (e.g., pooled HPLC fractions) from different class I molecules typically reveals a characteristic sequence motif for each class I allele.

Definition of motifs specific for different class I alleles allows the identification of potential peptide epitopes from an antigenic protein whose amino acid sequence is known. Typically, identification of potential peptide epitopes is initially carried out using a computer to scan the amino acid sequence of a desired antigen for the presence of motifs. The epitopic sequences are then synthesized. The capacity to bind MHC Class molecules is measured in a variety of different ways. One means is a Class I molecule binding assay as described in the related applications, noted above. Other alternatives described in the literature include inhibition of antigen presentation (Sette, et al., *J. Immunol.* 141:3893 (1991), *in vitro* assembly assays (Townsend, et al., *Cell* 62:285 (1990), and FACS based assays using mutated cells, such as RMA.S (Meliaf, et al., *Eur. J. Immunol.* 21:2963 (1991)).

Next, peptides that test positive in the MHC class I binding assay are assayed for the ability of the peptides to induce specific CTL responses *in vitro*. For instance, Antigen-presenting cells that have been incubated with a peptide can be assayed for the ability to induce CTL responses in responder cell populations. Antigen-presenting cells can be normal cells such as peripheral blood mononuclear cells or dendritic cells (Inaba, et al., *J. Exp. Med.* 166:182 (1987); Boog, *Eur. J. Immunol.* 18:219 [1988]).

Alternatively, mutant mammalian cell lines that are deficient in their ability to load class I molecules with internally processed peptides, such as the mouse cell lines RMA-S (Kärre, et al., *Nature*, 319:675 (1986); Ljunggren, et al., *Eur. J. Immunol.*

21:2963-2970 (1991)), and the human somatic T cell hybrid, T-2 (Cerundolo, et al., Nature 345:449-452 (1990)) and which have been transfected with the appropriate human class I genes are conveniently used, when peptide is added to them, to test for the capacity of the peptide to induce *in vitro* primary CTL responses. Other eukaryotic cell lines which could be used include various insect cell lines such as mosquito larvae (ATCC cell lines 5 CCL 125, 126, 1660, 1591, 6585, 6586), silkworm (ATTC CRL 8851), armyworm (ATCC CRL 1711), moth (ATCC CCL 80) and Drosophila cell lines such as a Schneider cell line (see Schneider J. Embryol. Exp. Morphol. 27:353-365 [1977]).

Peripheral blood lymphocytes are conveniently isolated following simple venipuncture or leukapheresis of normal donors or patients and used as the responder cell 10 sources of CTL precursors. In one embodiment, the appropriate antigen-presenting cells are incubated with 10-100 μ M of peptide in serum-free media for 4 hours under appropriate culture conditions. The peptide-loaded antigen-presenting cells are then 15 incubated with the responder cell populations *in vitro* for 7 to 10 days under optimized culture conditions. Positive CTL activation can be determined by assaying the cultures for the presence of CTLs that kill radiolabeled target cells, both specific peptide-pulsed targets as well as target cells expressing endogenously processed form of the relevant virus or tumor antigen from which the peptide sequence was derived.

Specificity and MHC restriction of the CTL is determined by testing against 20 different peptide target-cells expressing appropriate or inappropriate human MHC class I. The peptides that test positive in the MHC binding assays and give rise to specific CTL responses are referred to herein as immunogenic peptides.

The immunogenic peptides can be prepared synthetically, or by recombinant 25 DNA technology or from natural sources such as whole viruses or tumors. Although the peptide will preferably be substantially free of other naturally occurring host cell proteins and fragments thereof, in some embodiments the peptides can be synthetically conjugated to native fragments or particles.

The polypeptides or peptides can be a variety of lengths, either in their 30 neutral (uncharged) forms or in forms which are salts, and either free of modifications such as glycosylation, side chain oxidation, or phosphorylation or containing these modifications, subject to the condition that the modification not destroy the biological activity of the polypeptides as herein described.

Desirably, the peptide will be as small as possible while still maintaining substantially all of the biological activity of the large peptide. When possible, it may be desirable to optimize peptides of the invention to a length of 9 or 10 amino acid residues, commensurate in size with endogenously processed viral peptides or tumor cell peptides that are bound to MHC class I molecules on the cell surface.

Peptides having the desired activity may be modified as necessary to provide certain desired attributes, e.g., improved pharmacological characteristics, while increasing or at least retaining substantially all of the biological activity of the unmodified peptide to bind the desired MHC molecule and activate the appropriate T cell. For instance, the peptides may be subject to various changes, such as substitutions, either conservative or non-conservative, where such changes might provide for certain advantages in their use, such as improved MHC binding. By conservative substitutions is meant replacing an amino acid residue with another which is biologically and/or chemically similar, e.g., one hydrophobic residue for another, or one polar residue for another. The substitutions include combinations such as Gly, Ala; Val, Ile, Leu, Met; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe, Tyr. The effect of single amino acid substitutions may also be probed using D-amino acids. Such modifications may be made using well known peptide synthesis procedures, as described in e.g., Merrifield, Science 232:341-347 (1986), Barany and Merrifield, The Peptides, Gross and Meienhofer, eds. (N.Y., Academic Press), pp. 1-284 (1979); and Stewart and Young, Solid Phase Peptide Synthesis, (Rockford, Ill., Pierce), 2d Ed. (1984), incorporated by reference herein.

The peptides can also be modified by extending or decreasing the compound's amino acid sequence, e.g., by the addition or deletion of amino acids. The peptides or analogs of the invention can also be modified by altering the order or composition of certain residues, it being readily appreciated that certain amino acid residues essential for biological activity, e.g., those at critical contact sites or conserved residues, may generally not be altered without an adverse effect on biological activity. The non-critical amino acids need not be limited to those naturally occurring in proteins, such as L- α -amino acids, or their D-isomers, but may include non-natural amino acids as well, such as β - γ - δ -amino acids, as well as many derivatives of L- α -amino acids.

Typically, a series of peptides with single amino acid substitutions are employed to determine the effect of electrostatic charge, hydrophobicity, etc. on binding.

For instance, a series of positively charged (e.g., Lys or Arg) or negatively charged (e.g., Glu) amino acid substitutions are made along the length of the peptide revealing different patterns of sensitivity towards various MHC molecules and T cell receptors. In addition, multiple substitutions using small, relatively neutral moieties such as Ala, Gly, Pro, or 5 similar residues may be employed. The substitutions may be homo-oligomers or hetero-oligomers. The number and types of residues which are substituted or added depend on the spacing necessary between essential contact points and certain functional attributes which are sought (e.g., hydrophobicity versus hydrophilicity). Increased binding affinity for an MHC molecule or T cell receptor may also be achieved by such substitutions, 10 compared to the affinity of the parent peptide. In any event, such substitutions should employ amino acid residues or other molecular fragments chosen to avoid, for example, steric and charge interference which might disrupt binding.

Amino acid substitutions are typically of single residues. Substitutions, 15 deletions, insertions or any combination thereof may be combined to arrive at a final peptide. Substitutional variants are those in which at least one residue of a peptide has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the following Table 2 when it is desired to finely modulate the characteristics of the peptide.

TABLE 2

<u>Original Residue</u>	<u>Exemplary Substitution</u>
Ala	Ser
Arg	Lys, His
Asn	Gln
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	Lys; Arg
Ile	Leu; Val
Leu	Ile; Val
Lys	Arg; His
Met	Leu; Ile
Phe	Tyr; Trp
Ser	Thr
Thr	Ser
Trp	Tyr; Phe
Tyr	Trp; Phe
Val	Ile; Leu
Pro	Gly

Substantial changes in function (e.g., affinity for MHC molecules or T cell receptors) are made by selecting substitutions that are less conservative than those in Table 2, i.e., selecting residues that differ more significantly in their effect on maintaining (a) the structure of the peptide backbone in the area of the substitution, for example as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in peptide properties will be those in which (a) hydrophilic residue, e.g. seryl, is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a residue having an electropositive side chain, e.g., lysyl, 5 arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (c) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

The peptides may also comprise isosteres of two or more residues in the immunogenic peptide. An isostere as defined here is a sequence of two or more residues that can be substituted for a second sequence because the steric conformation of the first sequence fits a binding site specific for the second sequence. The term specifically includes peptide backbone modifications well known to those skilled in the art. Such modifications include modifications of the amide nitrogen, the α -carbon, amide carbonyl, complete replacement of the amide bond, extensions, deletions or backbone crosslinks.

20 See, generally, Spatola, Chemistry and Biochemistry of Amino Acids, peptides and Proteins, Vol. VII (Weinstein ed., 1983).

Modifications of peptides with various amino acid mimetics or unnatural amino acids are particularly useful in increasing the stability of the peptide *in vivo*. Stability can be assayed in a number of ways. For instance, peptidases and various 25 biological media, such as human plasma and serum, have been used to test stability. See, e.g., Verhoef et al., Eur. J. Drug Metab. Pharmacokin. 11:291-302 (1986). Half life of the peptides of the present invention is conveniently determined using a 25% human serum (v/v) assay. The protocol is generally as follows. Pooled human serum (Type AB, non-heat inactivated) is delipidated by centrifugation before use. The serum is then diluted 30 to 25% with RPMI tissue culture media and used to test peptide stability. At predetermined time intervals a small amount of reaction solution is removed and added to either 6% aqueous trichloracetic acid or ethanol. The cloudy reaction sample is cooled

(4°C) for 15 minutes and then spun to pellet the precipitated serum proteins. The presence of the peptides is then determined by reversed-phase HPLC using stability-specific chromatography conditions.

The peptides of the present invention or analogs thereof which have CTL stimulating activity may be modified to provide desired attributes other than improved serum half life. For instance, the ability of the peptides to induce CTL activity can be enhanced by linkage to a sequence which contains at least one epitope that is capable of inducing a T helper cell response. Particularly preferred immunogenic peptides/T helper conjugates are linked by a spacer molecule. The spacer is typically comprised of relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under physiological conditions. The spacers are typically selected from, e.g., Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer need not be comprised of the same residues and thus may be a hetero- or homo-oligomer. When present, the spacer will usually be at least one or two residues, more usually three to six residues. Alternatively, the CTL peptide may be linked to the T helper peptide without a spacer.

The immunogenic peptide may be linked to the T helper peptide either directly or via a spacer either at the amino or carboxy terminus of the CTL peptide. The amino terminus of either the immunogenic peptide or the T helper peptide may be acylated. Exemplary T helper peptides include tetanus toxoid 830-843, influenza 307-319, malaria circumsporozoite 382-398 and 378-389.

In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes CTL. Lipids have been identified as agents capable of priming CTL *in vivo* against viral antigens. For example, palmitic acid residues can be attached to the alpha and epsilon amino groups of a Lys residue and then linked, e.g., via one or more linking residues such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like, to an immunogenic peptide. The lipidated peptide can then be injected directly in a micellar form, incorporated into a liposome or emulsified in an adjuvant, e.g., incomplete Freund's adjuvant. In a preferred embodiment a particularly effective immunogen comprises palmitic acid attached to alpha and epsilon amino groups

of Lys, which is attached via linkage, e.g., Ser-Ser, to the amino terminus of the immunogenic peptide.

As another example of lipid priming of CTL responses, *E. coli* lipoproteins, such as tripalmitoyl-S-glycerylcysteinylseryl-serine (P₃CSS) can be used to prime virus specific CTL when covalently attached to an appropriate peptide. See, Deres et al., Nature 342:561-564 (1989), incorporated herein by reference. Peptides of the invention can be coupled to P₃CSS, for example, and the lipopeptide administered to an individual to specifically prime a CTL response to the target antigen. Further, as the induction of neutralizing antibodies can also be primed with P₃CSS conjugated to a peptide which displays an appropriate epitope, the two compositions can be combined to more effectively elicit both humoral and cell-mediated responses to infection.

In addition, additional amino acids can be added to the termini of a peptide to provide for ease of linking peptides one to another, for coupling to a carrier support, or larger peptide, for modifying the physical or chemical properties of the peptide or oligopeptide, or the like. Amino acids such as tyrosine, cysteine, lysine, glutamic or aspartic acid, or the like, can be introduced at the C- or N-terminus of the peptide or oligopeptide. Modification at the C terminus in some cases may alter binding characteristics of the peptide. In addition, the peptide or oligopeptide sequences can differ from the natural sequence by being modified by terminal-NH₂ acylation, e.g., by alkanoyl (C₁-C₂₀) or thioglycolyl acetylation, terminal-carboxyl amidation, e.g., ammonia, methylamine, etc. In some instances these modifications may provide sites for linking to a support or other molecule.

The peptides of the invention can be prepared in a wide variety of ways. Because of their relatively short size, the peptides can be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. See, for example, Stewart and Young, Solid Phase Peptide Synthesis, 2d. ed., Pierce Chemical Co. (1984), *supra*.

Alternatively, recombinant DNA technology may be employed wherein a nucleotide sequence which encodes an immunogenic peptide of interest is inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression. These procedures are generally known in the art,

as described generally in Sambrook et al., Molecular Cloning. A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor, New York (1982), which is incorporated herein by reference. Thus, fusion proteins which comprise one or more peptide sequences of the invention can be used to present the appropriate T cell epitope.

5 As the coding sequence for peptides of the length contemplated herein can be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci et al., J. Am. Chem. Soc. 103:3185 (1981), modification can be made simply by substituting the appropriate base(s) for those encoding the native peptide sequence. The coding sequence can then be provided with appropriate linkers and ligated into expression
10 vectors commonly available in the art, and the vectors used to transform suitable hosts to produce the desired fusion protein. A number of such vectors and suitable host systems are now available. For expression of the fusion proteins, the coding sequence will be provided with operably linked start and stop codons, promoter and terminator regions and usually a replication system to provide an expression vector for expression in the desired
15 cellular host. For example, promoter sequences compatible with bacterial hosts are provided in plasmids containing convenient restriction sites for insertion of the desired coding sequence. The resulting expression vectors are transformed into suitable bacterial hosts. Of course, yeast or mammalian cell hosts may also be used, employing suitable vectors and control sequences.

20 The peptides of the present invention and pharmaceutical and vaccine compositions thereof are useful for administration to mammals, particularly humans, to treat and/or prevent viral infection and cancer. Examples of diseases which can be treated using the immunogenic peptides of the invention include prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV and
25 condyloma acuminatum.

For pharmaceutical compositions, the immunogenic peptides of the invention are administered to an individual already suffering from cancer or infected with the virus of interest. Those in the incubation phase or the acute phase of infection can be treated with the immunogenic peptides separately or in conjunction with other treatments, as
30 appropriate. In therapeutic applications, compositions are administered to a patient in an amount sufficient to elicit an effective CTL response to the virus or tumor antigen and to cure or at least partially arrest symptoms and/or complications. An amount adequate to

accomplish this is defined as "therapeutically effective dose." Amounts effective for this use will depend on, e.g., the peptide composition, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician, but generally range for the initial immunization (that is for therapeutic or prophylactic administration) from about 1.0 μ g to about 5000 μ g of peptide for a 70 kg patient, followed by boosting dosages of from about 1.0 μ g to about 1000 μ g of peptide pursuant to a boosting regimen over weeks to months depending upon the patient's response and condition by measuring specific CTL activity in the patient's blood. It must be kept in mind that the peptides and compositions of the present invention may generally be employed in serious disease states, that is, life-threatening or potentially life threatening situations. In such cases, in view of the minimization of extraneous substances and the relative nontoxic nature of the peptides, it is possible and may be felt desirable by the treating physician to administer substantial excesses of these peptide compositions.

For therapeutic use, administration should begin at the first sign of viral infection or the detection or surgical removal of tumors or shortly after diagnosis in the case of acute infection. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter. In chronic infection, loading doses followed by boosting doses may be required.

Treatment of an infected individual with the compositions of the invention may hasten resolution of the infection in acutely infected individuals. For those individuals susceptible (or predisposed) to developing chronic infection the compositions are particularly useful in methods for preventing the evolution from acute to chronic infection. Where the susceptible individuals are identified prior to or during infection, for instance, as described herein, the composition can be targeted to them, minimizing need for administration to a larger population.

The peptide compositions can also be used for the treatment of chronic infection and to stimulate the immune system to eliminate virus-infected cells in carriers. It is important to provide an amount of immuno-potentiating peptide in a formulation and mode of administration sufficient to effectively stimulate a cytotoxic T cell response. Thus, for treatment of chronic infection, a representative dose is in the range of about 1.0 μ g to about 5000 μ g, preferably about 5 μ g to 1000 μ g for a 70 kg patient per dose.

Immunizing doses followed by boosting doses at established intervals, e.g., from one to four weeks, may be required, possibly for a prolonged period of time to effectively immunize an individual. In the case of chronic infection, administration should continue until at least clinical symptoms or laboratory tests indicate that the viral infection has been

5 eliminated or substantially abated and for a period thereafter.

The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral or local administration. Preferably, the pharmaceutical compositions are administered parenterally, e.g., intravenously, subcutaneously, intradermally, or intramuscularly. Thus, the invention provides compositions for

10 parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, e.g., water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be

15 packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, tonicity adjusting agents, wetting agents and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride,

20 calcium chloride, sorbitan monolaurate, triethanolamine oleate, etc.

The concentration of CTL stimulatory peptides of the invention in the pharmaceutical formulations can vary widely, i.e., from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, etc., in accordance with the particular mode of

25 administration selected.

The peptides of the invention may also be administered via liposomes, which serve to target the peptides to a particular tissue, such as lymphoid tissue, or targeted selectively to infected cells, as well as increase the half-life of the peptide composition. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals,

30 phospholipid dispersions, lamellar layers and the like. In these preparations the peptide to be delivered is incorporated as part of a liposome, alone or in conjunction with a molecule which binds to, e.g., a receptor prevalent among lymphoid cells, such as monoclonal

antibodies which bind to the CD45 antigen, or with other therapeutic or immunogenic compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the selected therapeutic/immunogenic peptide compositions. Liposomes for use in the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, e.g., liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, e.g., Szoka et al., Ann. Rev. Biophys. Bioeng. 9:467 (1980), U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369, incorporated herein by reference.

For targeting to the immune cells, a ligand to be incorporated into the liposome can include, e.g., antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, etc. in a dose which varies according to, *inter alia*, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

For aerosol administration, the immunogenic peptides are preferably supplied in finely divided form along with a surfactant and propellant. Typical percentages of peptides are 0.01%-20% by weight, preferably 1%-10%. The surfactant must, of course, be nontoxic, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight

of the composition, preferably 0.25-5%. The balance of the composition is ordinarily propellant. A carrier can also be included, as desired, as with, e.g., lecithin for intranasal delivery.

In another aspect the present invention is directed to vaccines which contain as an active ingredient an immunogenically effective amount of an immunogenic peptide as described herein. The peptide(s) may be introduced into a host, including humans, linked to its own carrier or as a homopolymer or heteropolymer of active peptide units. Such a polymer has the advantage of increased immunological reaction and, where different peptides are used to make up the polymer, the additional ability to induce antibodies and/or CTLs that react with different antigenic determinants of the virus or tumor cells. Useful carriers are well known in the art, and include, e.g., thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly(lysine:glutamic acid), influenza, hepatitis B virus core protein, hepatitis B virus recombinant vaccine and the like. The vaccines can also contain a physiologically tolerable (acceptable) diluent such as water, phosphate buffered saline, or saline, and further typically include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are materials well known in the art. And, as mentioned above, CTL responses can be primed by conjugating peptides of the invention to lipids, such as P₃CSS. Upon immunization with a peptide composition as described herein, via injection, aerosol, oral, transdermal or other route, the immune system of the host responds to the vaccine by producing large amounts of CTLs specific for the desired antigen, and the host becomes at least partially immune to later infection, or resistant to developing chronic infection.

Vaccine compositions containing the peptides of the invention are administered to a patient susceptible to or otherwise at risk of viral infection or cancer to elicit an immune response against the antigen and thus enhance the patient's own immune response capabilities. Such an amount is defined to be an "immunogenically effective dose." In this use, the precise amounts again depend on the patient's state of health and weight, the mode of administration, the nature of the formulation, etc., but generally range from about 1.0 μ g to about 5000 μ g per 70 kilogram patient, more commonly from about 10 μ g to about 500 μ g mg per 70 kg of body weight.

In some instances it may be desirable to combine the peptide vaccines of the invention with vaccines which induce neutralizing antibody responses to the virus of interest, particularly to viral envelope antigens.

For therapeutic or immunization purposes, nucleic acids encoding one or more of the peptides of the invention can also be administered to the patient. A number of methods are conveniently used to deliver the nucleic acids to the patient. For instance, the nucleic acid can be delivered directly, as "naked DNA". This approach is described, for instance, in Wolff *et. al.*, *Science* 247: 1465-1468 (1990) as well as U.S. Patent Nos. 5,580,859 and 5,589,466. The nucleic acids can also be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Particles comprised solely of DNA can be administered. Alternatively, DNA can be adhered to particles, such as gold particles. The nucleic acids can also be delivered complexed to cationic compounds, such as cationic lipids. Lipid-mediated gene delivery methods are described, for instance, in WO 96/18372; WO 93/24640; Mannino and Gould-Fogerite (1988) *BioTechniques* 6(7): 682-691; Rose U.S. Pat No. 5,279,833; WO 91/06309; and Felgner *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84: 7413-7414. The peptides of the invention can also be expressed by attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into an acutely or chronically infected host or into a noninfected host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits a host CTL response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848, incorporated herein by reference. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.* (*Nature* 351:456-460 (1991)) which is incorporated herein by reference. A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, e.g., *Salmonella typhi* vectors and the like, will be apparent to those skilled in the art from the description herein.

A preferred means of administering nucleic acids encoding the peptides of the invention uses minigene constructs encoding multiple epitopes of the invention. To create a DNA sequence encoding the selected CTL epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes are reverse translated. A human codon usage table is used to guide the codon choice for each amino acid. These epitope-encoding

DNA sequences are directly adjoined, creating a continuous polypeptide sequence. To optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequence that could be reverse translated and included in the minigene sequence include: helper T lymphocyte epitopes, a leader (signal) sequence, and an endoplasmic reticulum retention signal. In addition, MHC presentation of CTL epitopes may be improved by including synthetic (e.g. poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL epitopes.

The minigene sequence is converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) are synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides are joined using T4 DNA ligase. This synthetic minigene, encoding the CTL epitope polypeptide, can then be cloned into a desired expression vector.

Standard regulatory sequences well known to those of skill in the art are included in the vector to ensure expression in the target cells. Several vector elements are required: a promoter with a down-stream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (e.g. ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, e.g., the human cytomegalovirus (hCMV) promoter. See, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

Additional vector modifications may be desired to optimize minigene expression and immunogenicity. In some cases, introns are required for efficient gene expression, and one or more synthetic or naturally-occurring introns could be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences can also be considered for increasing minigene expression. It has recently been proposed that immunostimulatory sequences (ISSs or CpGs) play a role in the immunogenicity of DNA vaccines. These sequences could be included in the vector, outside the minigene coding sequence, if found to enhance immunogenicity.

In some embodiments, a bicistronic expression vector, to allow production of the minigene-encoded epitopes and a second protein included to enhance or decrease immunogenicity can be used. Examples of proteins or polypeptides that could beneficially

enhance the immune response if co-expressed include cytokines (e.g., IL2, IL12, GM-CSF), cytokine-inducing molecules (e.g. LeIF) or costimulatory molecules. Helper (HTL) epitopes could be joined to intracellular targeting signals and expressed separately from the CTL epitopes. This would allow direction of the HTL epitopes to a cell compartment different than the CTL epitopes. If required, this could facilitate more efficient entry of HTL epitopes into the MHC class II pathway, thereby improving CTL induction. In contrast to CTL induction, specifically decreasing the immune response by co-expression of immunosuppressive molecules (e.g. TGF- β) may be beneficial in certain diseases.

Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate *E. coli* strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping and DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as a master cell bank and a working cell bank.

Therapeutic quantities of plasmid DNA are produced by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate fermentation medium (such as Terrific Broth), and grown to saturation in shaker flasks or a bioreactor according to well known techniques. Plasmid DNA can be purified using standard bioseparation technologies such as solid phase anion-exchange resins supplied by Quiagen. If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffer saline (PBS). A variety of methods have been described, and new techniques may become available. As noted above, nucleic acids are conveniently formulated with cationic lipids. In addition, glycolipids, fusogenic liposomes, peptides and compounds referred to collectively as protective, interactive, non-condensing (PINC) could also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

Target cell sensitization can be used as a functional assay for expression and MHC class I presentation of minigene-encoded CTL epitopes. The plasmid DNA is

introduced into a mammalian cell line that is suitable as a target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation. Electroporation can be used for "naked" DNA, whereas cationic lipids allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be 5 co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). These cells are then chromium-51 labeled and used as target cells for epitope-specific CTL lines. Cytolysis, detected by ^{51}Cr release, indicates production of MHC presentation of minigene-encoded CTL epitopes.

In vivo immunogenicity is a second approach for functional testing of minigene 10 DNA formulations. Transgenic mice expressing appropriate human MHC molecules are immunized with the DNA product. The dose and route of administration are formulation dependent (e.g. IM for DNA in PBS, IP for lipid-complexed DNA). Twenty-one days after immunization, splenocytes are harvested and restimulated for 1 week in the presence of peptides encoding each epitope being tested. These effector cells (CTLs) are assayed 15 for cytolysis of peptide-loaded, chromium-51 labeled target cells using standard techniques. Lysis of target cells sensitized by MHC loading of peptides corresponding to minigene-encoded epitopes demonstrates DNA vaccine function for *in vivo* induction of CTLs.

Antigenic peptides may be used to elicit CTL *ex vivo*, as well. The resulting 20 CTL, can be used to treat chronic infections (viral or bacterial) or tumors in patients that do not respond to other conventional forms of therapy, or will not respond to a peptide vaccine approach of therapy. *Ex vivo* CTL responses to a particular pathogen (infectious agent or tumor antigen) are induced by incubating in tissue culture the patient's CTL precursor cells (CTLp) together with a source of antigen-presenting cells (APC) and the 25 appropriate immunogenic peptide. After an appropriate incubation time (typically 1-4 weeks), in which the CTLp are activated and mature and expand into effector CTL, the cells are infused back into the patient, where they will destroy their specific target cell (an infected cell or a tumor cell).

The peptides may also find use as diagnostic reagents. For example, a peptide 30 of the invention may be used to determine the susceptibility of a particular individual to a treatment regimen which employs the peptide or related peptides, and thus may be helpful in modifying an existing treatment protocol or in determining a prognosis for an affected

individual. In addition, the peptides may also be used to predict which individuals will be at substantial risk for developing chronic infection.

The following example is offered by way of illustration, not by way of limitation.

5

Example 1

Class I antigen isolation was carried out as described in the related applications, noted above. Naturally processed peptides were then isolated and sequenced as described there. An allele-specific motif and algorithms were determined and quantitative binding assays were carried out.

10

Using the motifs identified above for various HLA alleles, amino acid sequences from a number of antigens were analyzed for the presence of these motifs.

Tables 3- ** provide the results of these searches.

15

The above examples are provided to illustrate the invention but not to limit its scope. Other variants of the invention will be readily apparent to one of ordinary skill in the art and are encompassed by the appended claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference.

20

Table 3

25

30

Sequence	Antigen	Molecule
FTFSPTYKAPLSK	HBV	POL
GTLQPQEHIVLKLK	HBV	POL
FTFSPTYKAPLCK	HBV	POL
GTLQPQEHIVLKIK	HBV	POL
LVVSYVNNTNMGLK	HBV	POL
STTDLEAYFKDCLFK	HBV	X
LVVSYVNVNMGGLK	HBV	NUC
GTLQPQDHIVQKIK	HBV	POL
STSSCLHQSAVRK	HBV	POL
TTVNAHQILPKVLHK	HBV	X
RTPARVTGGVFLVDK	HBV	POL

Sequence	Antigen	Molecule
HTTNFASK	HBV ayw	
PTFSPTYK	HBV ayw	
PTYKAFLCKOY	HBVayw	
CTTPAQGTSMY	HBVayw	
PTSCPPTCPGY	HBVayw	
FSQFSRGNY	HBVayw	
LMPLYACIQSK	HBVayw	
RVTGGVFLVDK	HBVayw	POL
HTLWKAGILYK	HBVayw	
QTRHYLHTLWK	HBVayw	
GTDNSVVLSRK	HBVayw	
SYVNTNMGLKF	HBVayw	
LYSILSPF	HBVayw	
WYWGPSLYSIL	HBVayw	
LYSILSPFLPL	HBVayw	
PYKEFGATVEL	HBVayw	
CTWMNSTGFTK	HCV	
MYVGDLCGSVF	HCV	
VYLLPRRGPRL	HCV	
ITKIQQNFRVYY	HIV	
KVYLAWVPAHK	HIV	
KMIGGIGGGFIK	HIV	
IVASCDKCOLK	HIV	
KVKQWPLTEEK	HIV	
TVNDIQKLVGK	HIV	
DVKOLTEAVQK	HIV	
AVVIQDNSDIK	HIV	
WTYQIYQEPFK	HIV	
VTVYYGVFWK	HIV	
LTEDRWNKPQK	HIV	
ATDIQTKELOK	HIV	
OTKELOKOITK	HIV	

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Sequence	Antigen	Molecule
WTVQPIVLPEK	HIV	
QVPLRPMTYK	HIV nef 73-82	
QVPLYPMTFK	HIV nef 73-82	
VPLRPMTYK	HIV nef 74-82	
AVDLYHFLK	HIV nef 84-94	
AVDLSHFLK	HIV nef 84-94	
ATLYCVHQR	HIV, p17, 82-90	
RLRDLLLIV	HIV-1 NL43 768-776	
RLRDLLLIVTR	HIV-1 NL43 768-778	
RLRDYLLIVTR	HIV-1 NL43 768-778	
LRDLLLIVTR	HIV-1 NL43 769-778	
QIYQEPFKNLK	HIV-1 RT 507-517	
AVFTIHNFK	HIVcon	
RTLNAAWK	HIVcon	
ETAYF1LK	HIVcon	
RLRPGGKKK	HIVgag p17/2	
KIRLRPGGKK	HIVgag p17/2	
KIRLRPGGK	HIVgag p17/2	
ETTDLYCY	HPV16	E7
GTLGIVCPICSQK	HPV16	E7

Sequence	Antigen	Molecule
LMGTLGIVCPICSQK	HPV16	E7
AVCDKCLK	HPV16	E6
PYAVCDKCLKF	HPV16	E6
HYCYSLYGTTL	HPV16	E6
FYSRIREL	HPV16	E6
TLEKLINTGLY	HPV18	E6
KTVLELTEVFEFAFK	HPV18	E6
TMLCMCCK	HPV18	E7
NTSLQDIEITCVYCK	HPV18	E6
EVFEFAFK	HPV18	E6
KQSSKALQR	Leukemia	b3A2 CMI
ATGFKQSSK	Leukemia	b3A2 CMI
HSATGFKQSSK	Leukemia	b3A2 CMI
FKQSSKALQR	Leukemia	b3A2 CMI
VTCLGLSY	MAGE1	
ITKKVADLVGFLLLK	MAGE1	
LVGFLLLK	MAGE1	
VTKAEMLESVIKNYK	MAGE1	
TSCILESILFR	MAGE1	
NYKHCPEI	MAGE1	
SYVLVTCL	MAGE1	
ETDPISHTY	MAGE1 (a)	
ETDPTSHLY	MAGE1 (a)	
ETDPTSNTY	MAGE1 (a)	
ETDPTSHVY	MAGE1 (a)	
ETDPTSHSY	MAGE1 (a)	
ETDPASHTY	MAGE1 (a)	
EVDPTSHTY	MAGE1 (a)	
ETDPTGHTY	MAGE1 (a)	
ETDRTSHTY	MAGE1 (a)	
EADPTSHTY	MAGE1 (a)	
ETVPTSHTY	MAGE1 (a)	

Sequence	Antigen	Molecule
ETDPPTSHTY	MAGE1 consensus	
ETDPPTGHSY	MAGE1 T(a)	
MFPDLESEF	MAGE2	
TTINYTLWR	MAGE2	
VIFSKASEY	MAGE2	
LVHFLLLKY	MAGE2	
LVHFLLLKY	MAGE2	
LVHFLLLKYR	MAGE2	
PVIFSKASEY	MAGE2	
STTINYTLWR	MAGE2	
VVEVVPISH	MAGE2	
EYLQLVFGI	MAGE2	
IFSKASEYL	MAGE2	
SFSTTINYTL	MAGE2	
LYILVTCCLG	MAGE2	
FATCLGLSY	MAGE3	
VVGNWQYFFPVIFSK	MAGE3	
LIIVLAIIR	MAGE3	
YFFPVIFSK	MAGE3	
NWQYFFPV	MAGE3	
NWQYFFPVIF	MAGE3	
IFSKASSSL	MAGE3	
EVDPTSNTY	MAGE41	
RYPLTFGWCY	nef/182	
RYPLTFGWC	nef/182	
ATQIPSYK	PAP	
LTELIFER	PAP	
HSFPHPLY	PSA	
TOEPALGTCY	PSA	
VTKFMLCAGRWTGGK	PSA	
HVISNDVCAQVHPQK	PSA	

Sequence	Antigen	Molecule
LYDMSLLKNRF	PSA	
ETDPTGHSTY	T2 analog of MAGE-3	

Table 4

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.000	ILDDMLILLY	9	c-ERB2			42		91		0.037	0.0012	
1.004	LLDDDETEY	9	c-ERB2			469		1	76		0.0038	0
1.005	GTQJFEDNY	9	c-ERB2			104		0.18		0	0.0031	
1.005	LTCSRQEPEY	9	c-ERB2			1131		0.13		0	0.0061	
1.007	ETLEIETGY	9	c-ERB2			401		1	0.03	<0.0002	<0.0002	
1.038	QLVQLQMLPY	9	c-ERB2			795		1	0.0021	0.011	0.0038	
1.074	PRHGSQDWSY	10	c-ERB2			899		27		0.0005	0.0005	
1.074	RLLDDETEY	10	c-ERB2			868		1	13	0.0017	0	
1.075	TELEETGY	10	c-ERB2			402		1	11	0	0	
1.077	YTMAGIGSPY	10	c-ERB2			772		1	11	0	0.010	0.012
1.078	GTPIAENPEY	10	c-ERB2			1229		1	0.063	<0.0002	0.0022	
1.074	RVLQGQJPNEY	10	c-ERB2			545		1	<0.0015	0.005	0.0050	
1.076	LQARNPQLCY	10	c-ERB2			154		1	0.020	0.0012	<0.0002	
1.069	WVQGMFLTY	10	c-ERB2			55		1	0.018	0.0024	0.011	
1.076	MGDLVILAEY	10	c-ERB2			1014		1	0.012	<0.002	<0.002	
1.103	KDRTTMMR	9	c-ERB2			681		3.11		0.76	0.0016	
1.107	WVQGMJRK	9	c-ERB2			659		3.11		0.11	0.22	
1.064	LVESPRHVK	9	c-ERB2			852		3.11		0.48	0.070	
1.053	VLKENTSPK	9	c-ERB2			754		3.11		0.40	0.013	
1.059	ILIKRKKQK	9	c-ERB2			673		3.11		0.38	0.0097	
1.051	ILWKDQPHK	9	c-ERB2			167		3.11		0.29	0.31	
1.103	KTMDPCLAR	9	c-ERB2			860		3.11		0.17	0.24	
1.069	GWVCLIK	9	c-ERB2			668		3.11		0.0047	0.009	
1.059	QVCTGCTMK	9	c-ERB2			24		3.11		0.0007	0.002	
1.101	LLDRVQDVR	9	c-ERB2			806		3.11		0.007	<0.0005	
1.105	CYKCSQFLR	9	c-ERB2			528		3.11		0.0013	0.001	
1.103	TVCAGGCAR	9	c-ERB2			218		3.11		0.0004	0.0023	
1.051	ILKETELRK	9	c-ERB2			714		3.11		0.019	0.0023	
1.024	VTAEDGTR	9	c-ERB2			322		3.11		<0.0002	0.014	
1.026	DLSYMPWIK	9	c-ERB2			607		3.11		0.0005	0.010	
1.077	TLMKQDFIK	10	c-ERB2			166		3.11		0.003	3.6	
1.072	GTQRCRCSK	10	c-ERB2			327		3.11		0.021	0.61	
1.076	KVLRDNTSPK	10	c-ERB2			751		3.11		0.38	0.72	
1.072	QLSLTELK	10	c-ERB2			161		3.11		0.20	0.013	
1.102	RLVHRDQAA	10	c-ERB2			801		3.11		0.18	0	
1.071	UNWGMQIAK	10	c-ERB2			822		3.11		0.14	0.4	
1.072	TIVYNNMVK	10	c-ERB2			948		3.11		0.013	0.12	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0731	RILKETELKK	10	c-ERB2			713	3.11	---	0.057	0.11	---	---
1.0745	VLVKSINNIW	10	c-ERB2			851	3.11	---	0.067	0.0077	---	---
1.1131	SVIFQNLQVIR	10	c-ERB2			423	3.11	---	0.017	0.075	---	---
1.1133	ITIVPMWQQLR	10	c-ERB2			478	3.11	---	0.0055	0.072	---	---
1.1127	ILKGGVUQQR	10	c-ERB2			148	3.11	---	0.040	0.0005	---	---
1.1143	LVSEFPRMAR	10	c-ERB2			972	3.11	---	0.0072	0.033	---	---
1.1136	GYVFCILIKR	10	c-ERB2			668	3.11	---	0.018	0.033	---	---
1.0726	CVARCPSCVK	10	c-ERB2			596	3.11	---	0.022	0.0042	---	---
1.1137	WVCFILKRR	10	c-ERB2			669	3.11	---	0.0030	0.016	---	---
1.0728	GILIKRKRQK	10	c-ERB2			672	3.11	---	0.015	0.0014	---	---
1.1129	RTVCAGGCAR	10	c-ERB2			217	3.11	---	0.0068	0.013	---	---
1.1134	GLACHQLCAR	10	c-ERB2			508	3.11	---	0.011	0	---	---
1.1139	KIPVAIKVLR	10	c-ERB2			747	3.11	---	0.0009	0.0099	---	---

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0291	VCEADYYFEY	9	EBNA1			499	1	0.016				
1.0295	— PILRESIVC	9	EBNA1			503	1	0.010				
1.0681	IVGCEADYYFEY	10	EBNA1			498	1	0.015				
1.0689	GTWVACVFEY	10	EBNA1			501	1	0.014				
1.0793	GVFVYCCSK	9	EBNA1			506	3.11	0.30	0.61			
1.1016	KTSLYNLR	9	EBNA1			514	3.11	0.31	0.12			
1.0297	AIKDLVMTK	9	EBNA1			578	3.11	0.046	0.034			
1.0687	QTH-HFAEVLK	10	EBNA1			567	3.11	0.010	0.21			
1.1124	GTALALIPOCR	10	EBNA1			523	3.11	0.0028	0.056			

Pepptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
5.005	CTEIKLSDY	9	FLU	A	NP	44	1	3.6				
5.006	STLELRSRY	9	FLU	A	NP	377	1	0.020				
5.004	ILRGCSVAHK	9	FLU	A	NP	265	3				1.5	0.0087
5.001	RMCNLLKKK	9	FLU	A	NP	221	3				0.27	0.062
5.0051	LMQESTLIR	9	FLU	A	NP	166	3				0.031	0.10
5.006	MIDGICRFY	9	FLU	A	NP	32	3				0.059	0.0010
5.008	MVLSAFDDE	9	FLU	A	NP	66	3				0.0016	0.001
5.009	YRQMCTELK	9	FLU	A	NP	40	3				0.0031	0.030
5.004	YRQMCTELK	9	FLU	A	NP	200	3				0.0028	0.024
5.002	GRDRNHWK	9	FLU	A	NP	165	3				0.12	0.84
5.010	SLMQGSTLPR	10	FLU	A	NP	31	3				0.50	0.079
5.005	KMIDGICRFY	10	FLU	A	NP	264	3				0.36	0.037
5.006	ILRGCSVAK	10	FLU	A	NP	175	3				0.019	0.0066
5.0102	RSCAACAAVK	10	FLU	A	NP	376	3				0.0016	0.016
5.0105	STLELRSRY	10	FLU	A	NP	382	3				0.012	0
5.0103	RSRTWAIIRR	10	FLU	A	NP	65	3				0.0014	0.010
5.0101	MVLSAFDDE	10	FLU	A	NP	39	24				2.9	
5.0061	PRQMCTEL	9	FLU	A	NP	218	24				0.031	
5.0060	AYERMONIL	9	FLU	A	NP	38	24				0.15	
5.0112	RFTIQMCTEL	10	FLU	A	NP							

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A21	A32	A11	A24
1.0155	LLDTASALY	9	HBV	adr	CORE	420	-1	25	0.0007	0		
1.0166	SLDVSAAFY	9	HBV	adr	TL	101	-1	172	0.0037	0.0006		
2.0125	PTGCRTSLY	9	HBV	ALL		1,382	-1	13	0.0008	0		
2.0126	MSTTDLEAY	9	HBV	adr	POL	1,382	-1	0.85	<0.0008	0		
1.0208	PTGCRTSLY	9	HBV	adr	POL	1,280	-1	0.77	0	0		
1.0387	LTKQYUNLY	9	HBV	adr	POL	1,280	-1	0.50	0.0003	0.0075		
1.0166	KVGNFTGLY	9	HBV	adr	POL	629	-1	0.68	0.30	0.014		
2.0122	MSPTDLEAY	9	HBV	adr		1,550	-1	0.67				
2.0120	PSQPSKIGNY	9	HBV	sym		984	-1	0.57				
2.0112	PSQWAFAKY	9	HBV	adr		316	-1	0.54				
2.0119	QSAVAKAY	9	HBV	adr		881	-1	0.25				
1.0174	PLDKGKPY	9	HBV	adr	POL	698	-1	0.019	<0.0002	<0.0002		
1.0378	SLMLYKTY	9	HBV	adr	POL	1072	-1	0.017				
2.0115	ASRDQWVSY	9	HBV	sym		499	-1	0.013				
2.0124	PSRGKGLY	9	HBV	adr/adr		1,364	-1	0.011				
2.0121	SSTSRNNTY	9	HBV	adr		1,036	-1	0.0097				
1.0519	DLDTASALY	10	HBV	adr	CORE	419	-1	11.1	0	0		
1.0513	LLDPRVRGLY	10	HBV	adr	ENV	120	-1	6.3	0.17	0		
2.0239	LSLDVSAAFY	10	HBV	ALL		1,000	-1	4.2	<0.0009	0.0037		
1.0911	PLQQQVHLY	10	HBV	adr	POL	1,250	-1	1.1	0.0023	0.014	0.0048	0.0017
2.0216	QTPGAKLHLY	10	HBV	sym	POL	1087	-1	1.1	0.0056	0.012		
2.0224	KTGAKLHLY	10	HBV	adr		1,098	-1	0.69	0.0003	0.59	0.22	0
1.0291	KTGAKLHLY	10	HBV	adr	POL	1098	-1	0.57	0.0020	0.53	0.35	0.001
2.0242	QTPGAKLHLY	10	HBV	sym		1,087	-1	0.37	0.0057	0.011		
1.0556	KTGAKLHLY	10	HBV	adr	POL	1089	-1	0.34	0.0023	0.004	0.090	0
2.0241	KTGAKLHLY	10	HBV	adr		1,069	-1	0.30	0.0027	0.15	0.095	0
1.0766	LQDPVRVLY	10	HBV	adr	ENV	120	-1	0.21	0.014	0		
1.0806	TTPAQCTSMY	10	HBV	adr		288	-1	0.20	0	0		
2.0240	LSSTSRNNTY	10	HBV	adr		1,035	-1	0.20	<0.0009	0		
1.0511	PLDKGKPY	10	HBV	adr	POL	698	-1	0.16	0	0		
2.0238	HSASFCPSY	10	HBV	sym		767	-1	0.15	0	0.019	0.017	0
1.0795	FLTKQYUNLY	10	HBV	adr	POL	1,279	-1	0.12	0	0		
2.0237	RSASFCPSY	10	HBV	adr/adr		738	-1	0.11	0	0.033	0.020	0
1.0774	WLWGMIDRY	10	HBV	adr	CORE	416	-1	0.081	<0.0002	<0.0002		
2.0233	TTPAQCTSMY	10	HBV	sym		288	-1	0.068				
1.0542	ITLUWKGAGLY	10	HBV	adr	POL	723	-1	0.030				
2.0231	TSQTPPICPY	10	HBV	adr		226	-1	0.018				

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
2.0046	KSVQILLESLY	10	HBV	active	POL	1161	1	0.016				
1.0910	NLVPSLLV	10	HBV	adv	POL	1059	1	0.015				
2.0089	LLYQTCRK	9	HBV	adv	POL	1044	3				1.8	0.64
2.0016	IMPRARYPK	9	HBV	adv	POL	713	3				0.99	1.5
2.0082	CLJQSPVKE	9	HBV	adv	POL	867	3				0.14	0.025
5.0066	SACISVWR	9	HBV	adv	POL	531	3				40.0000	0.067
2.0077	HLHQDQIKK	9	HBV	adv	POL	686	3				0.041	0.0075
2.0019	SLPQEHIQK	10	HBV	adv	POL	1157	3				0.36	4.2
2.0024	SMHPSCCCTK	10	HBV	adv/adv	POL	295	3				0.43	1.9
2.0025	SMHPSCCCTK	10	HBV	adv	POL	295	3				1.1	1.79
5.007	QAFPSPTYK	10	HBV	adv	POL	665	3				0.15	1.3
2.0014	LLVYQTCRK	10	HBV	adv	POL	1033	3				0.09	0.021
2.0045	YMDDDVVLGAK	10	HBV	adv	POL	1123	3				0.16	0.0076
5.0008	TSACISVWR	10	HBV	adv	POL	530	3				0.0006	0.013
2.0084	PTTAAPICK	9	HBV	adv	POL	1263	11				0.030	0.065
2.0054	PTDIEHAYRK	9	HBV	adv	"X"	1552	11				0.0002	0.016
2.0051	KYTSQSPWLL	9	HBV	ALL		1,330	24					3.6
2.0059	LYAAVAVINFL	9	HBV	adv		1,169	24					3.2
2.0064	PTTAAPICK	9	HBV	adv		659	24					2.1
2.0005	LYSTVTPR	9	HBV	adv/adv		655	24					1.9
2.0048	FPKVKTKL	9	HBV	adv		718	24					1.7
2.0019	FPKVKTKL	9	HBV	adv		718	24					1.6
2.0039	LTSILSPFL	9	HBV	adv		369	24					0.50
2.0064	LYSTVTPR	9	HBV	adv		656	24					0.57
2.0003	LYNLSLSPF	9	HBV	adv		368	24					0.24
2.0051	NYRVSWPKP	9	HBV	adv		991	24					0.18
2.0050	HYRQTRHML	9	HBV	adv/adv		733	24					0.15
2.0007	HYFKTRHML	9	HBV	adv		714	24					0.057
2.0060	GTPLALMPL	9	HBV	ALL		1,224	24					0.049
5.0062	ATPPTPNAPI	9	HBV	ALL	NUCLEUS	131	24					0.026
2.0054	LYQTCRK	9	HBV	adv		1,085	24					0.014
2.0043	SYOHFRKLL	9	HBV	adv		607	24					0.011
2.0181	LYSHPMLGP	10	HBV	ALL		1,077	24					1.1
2.0182	LYAAVAVINFL	10	HBV	adv		1,169	24					0.32
2.0188	LYRPLSLIP	10	HBV	adv		1,271	24					0.25
2.0174	SYQIFRKLL	10	HBV	adv/adv		607	24					0.16
2.0173	SYQIFRKLL	10	HBV	adv/adv		578	24					0.066

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A21	A32	A11	A24
2.076	YVTFELILVHIV	10	HBV	adr	SYW	715	24	0.040	0.022
2.077	AYTREPNAPL	10	HBV	adr	YLL	521	24	0.011	0.011
2.071	GYRWMCILRIF	10	HBV	adr	YLL	234	24	0.009	0.009
5.015	NPLISLGHL	10	HBV	adr	YOL	572	24
5.077	YVSEMLLYK	9	HBV	adr	YOL	1090	3,11
1.089	LLVAKFAGK	9	HBV	adr	POL	1064	3,11
1.089	LLVAKFAGK	9	HBV	adr	POL	1095	3,11
1.0570	VTKYPLDK	9	HBV	adr	POL	722	3,11	0.004	0.13
1.0176	RHYLHLTLWK	9	HBV	adr	POL	719	3,11	0.010	0.010
1.0367	STVSEHNPK	9	HBV	adr	POL	668	3,11	0.021	0.009
1.0219	TTDQDAPK	9	HBV	adr	TX	1523	3,11	0.006	0.02
1.0648	YVSEMLLYK	9	HBV	adr	POL	1061	3,11	0.39	0.92
1.0263	PTYKAPLTK	9	HBV	adr	POL	1274	3,11	0.17	0.71
1.0967	HLVYVAVR	9	HBV	adr	POL	1257	3,11	0.54	0.000
1.0358	STNRQLGK	9	HBV	adr	ENV	85	3,11	0.51	0.34
1.0991	ALRFSKAK	9	HBV	adr	TX	1688	3,11	0.44	<0.0005
1.0177	PVNRPIDWK	9	HBV	adr	POL	1197	3,11	0.000	0.41
1.0369	TVNEMRKL	9	HBV	adr	POL	703	3,11	0.016	0.40
1.1011	WNVHYTROT	9	HBV	adr	POL	740	3,11	0.000	0.33
1.0152	STTSIGCK	9	HBV	adr	ENV	277	3,11	0.011	0.29
1.0213	QVLPKHLHK	9	HBV	adr	TX	1505	3,11	0.10	0.28
1.0172	LTKYPLDK	9	HBV	adr	POL	693	3,11	0.069	0.23
1.0374	CLHQSAVRK	9	HBV	adr	POL	870	3,11	0.22	0.017
1.0880	WDPDSQSK	9	HBV	adr	POL	963	3,11	0.011	0.20
1.0382	PLVACQAK	9	HBV	adr	POL	1259	3,11	0.18	0.004
2.0074	YVNTNIMGK	9	HBV	adr	CORE	507	3,11	0.16	0.008
1.0199	PLVACQSK	9	HBV	adr	POL	1230	3,11	0.11	0.018
1.0972	RLADEGUNR	9	HBV	adr	POL	601	3,11	0.10	0.025
1.0976	AVNHYFKR	9	HBV	adr	POL	711	3,11	0.0071	0.008
1.0975	RKXKIMP	9	HBV	adr	POL	680	3,11	0.005	0.0002
1.0977	ILYKRETR	9	HBV	adr	POL	730	3,11	0.005	<0.0005
1.0993	KYTVLGGCR	9	HBV	adr	-X-	1548	3,11	0.042	0.082
1.0165	YVSPFWTHK	9	HBV	adr	POL	821	3,11	0.072	0.076
1.0982	LLVYKFGK	9	HBV	adr	POL	1085	3,11	0.072	0.005
1.0978	RLVQQTSTK	9	HBV	adr	POL	757	3,11	0.068	0.002
1.0219	PVLGCCRHK	9	HBV	adr	-X-	1550	3,11	0.055	0.019
1.1042	RLVQQTSTK	9	HBV	adr	POL	766	3,11	0.064	0.002

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.1043	MLLIVKTYGR	9	HBV	adv	POL	1094	3.11		0.061	0.0032		
1.0770	TYNEEKRRK	9	HBV	adv	POL	674	3.11		0.048	0.037		
1.1043	NLYFVAVOR	9	HBV	adv	POL	1286	3.11		0.042	0.0011		
1.1046	LYTAPTCGR	9	HBV	adv	POL	1407	3.11		0.021	0		
1.0845	LVSGCIVWIR	9	HBV	adv	CORE	509	3.11		0.0033	0.020		
1.0861	LVCGSGGLPR	9	HBV	adv	POL	1022	3.11		0.008	0.015		
1.0567	HISCLTCGR	9	HBV	adv	CORE	494	3.11		0.013	0.011		
1.1047	SVPSRLPDR	9	HBV	adv	POL	1424	3.11		0.007	0.010		
1.0869	SVPSHLUPDR	9	HBV	adv	POL	1395	3.11		0.004	0.010		
1.0564	TILQG&HVLK	10	HBV	adv	POL	1175	3.11		0.072	5.6		
2.0005	TWPPVPHWIK	10	HBV	adv	POL	669	3.11		0.057	4.2		
1.0543	TEWKAGILRK	10	HBV	adv	POL	724	3.11		3.5	1.0		
1.0807	SMYFSCCTK	10	HBV	adv	ENV	295	3.11		1.5	3.4		
1.1153	RLLPAPTCGR	10	HBV	adv	POL	1406	3.11		2.8	0.130		
1.0584	STTDLAEATK	10	HBV	adv	X	1522	3.11		0.006	2.7		
1.0564	LLIYKTPRK	10	HBV	adv	POL	1065	3.11		2.5	0.012		
1.0799	TYNAHAEHNLK	10	HBV	adv	X	1529	3.11		0.82	0.65		
1.0566	EVYFKDCLK	10	HBV	adv	X	157	3.11		0.037	0.74		
1.1081	LWDPSQPSK	10	HBV	adv	POL	962	3.11		0.009	0.63		
1.0769	MLLIVKTYGR	10	HBV	adv	POL	1094	3.11		0.61	0.020		
1.0546	TATPSLSTK	10	HBV	adv	POL	859	3.11		0.26	0.092		
1.0562	SLGCHLUNPK	10	HBV	adv	POL	1150	3.11		0.20	0.078		
1.1152	RLLGTYRPLK	10	HBV	adv	POL	1397	3.11		0.19	0.009		
1.0547	VTGCGFLVVK	10	HBV	adv	POL	943	3.11		0.035	0.17		
1.1150	RKIKPKTRPK	10	HBV	adv	POL	962	3.11		0.17	0.002		
1.0561	TYNGHQVLPK	10	HBV	adv	X	1500	3.11		0.073	0.092		
1.1091	SLPQQPTGCR	10	HBV	adv	POL	1377	3.11		0.077	0.043		
1.1072	TLPETTVRR	10	HBV	adv	CORE	532	3.11		<0.0003	0.075		
1.1089	GTONSVLRL	10	HBV	adv	POL	1320	3.11		0.025	0.072		
1.1171	STLPEETTVRK	10	HBV	adv	CORE	531	3.11		0.005	0.048		
2.0210	KVTKYLPDK	10	HBV	adv	POL	721	3.11		0.027	0.053		
1.1148	STTHGDKPSR	10	HBV	adv	POL	702	3.11		0.057	0.038		
1.0935	VLSCWHLQPK	10	HBV	adv	POL	923	3.11		0.029	0.067		
1.0761	NVTKYLPDK	10	HBV	adv	POL	721	3.11		<0.0004	0.023		
1.1092	RVCCQOLDPSR	10	HBV	adv	X	1422	3.11		0.019	0.022		
1.0793	SLGCHLUNPK	10	HBV	adv	POL	1179	3.11		0.017	0.014		
1.0919	VLSCWHLQPK	10	HBV	adv	CORE	531	3.11		0.015	0.007		

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
2.0017	FVCPPLTVNEK	10	HBV	ayw	POL	698	3.11		0.0057	0.0015		
1.0535	YVCPLTVNEK	10	HBV	adr	POL	669	3.11		0.0069	0.014		
1.1075	RLADEGLNRR	10	HBV	adr	POL	601	3.11		0.013	0.0004		
1.1066	IVLKLIKQCFR	10	HBV	adr	POL	1185	3.11		0.013	0.0024		
1.0773	PIFSSWAFAK	10	HBV	adr	ENV	314	3.11		<0.0003	0.010		
1.0778	LTVNENRLK	10	HBV	adr	POL	702	3.11		0.0025	0.0095		

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0118	CTCROSSDLY	9	HCV		LORF	1123	1	3.0	0	0.010		
1.0112	NIVDVQVLY	9	HCV		NS1/ENV2	697	1	0.60	0	0.010		
2.0024	VQDQNQSY	9	HCV			302	1	0.54		0.0005	0.0003	
2.0035	LTPKQMDY	9	HCV			605	1	0.078				
1.0145	RVCEKMLY	9	HCV		LORF	2588	1	0.053				
1.0140	DWVCGSMY	9	HCV		LORF	2416	1	0.039				
2.0036	FTPKKIRMY	9	HCV			636	1	0.012				
1.0529	GLSAFSLHSY	10	HCV		LORF	2888	1	0.41	0.0002	0.013	0.0034	0.0002
1.0489	TLHGCPNPLY	10	HCV		LORF	1617	1	0.30	0.11	0.0024		
2.0037	EVVLLFLL	9	HCV			719	24				1.4	
2.0069	MVVGGEVHRL	10	HCV			633	24				0.026	
2.0120	EVVLLFLL	10	HCV			719	24				0.010	
1.0139	SVPAEIRK	9	HCV		LORF	2269	3,11		0.016	0.07		
1.0953	QLFTPSPR	9	HCV		ENV1	290	3,11		0.75	0.033		
1.0090	RIGVRAATRK	9	HCV		CORE	43	3,11		0.74	0.16		
1.0123	LIFCHSKCK	9	HCV		LORF	1391	3,11		0.54	0.19		
1.0122	HURCHSKK	9	HCV		LORF	1390	3,11		0.25	0.010		
1.0952	KTSRSQPR	9	HCV		CORE	51	3,11		0.16	0.064		
1.0120	AVCTRGVAK	9	HCV		LORF	1183	3,11		0.016	0.038		
1.0143	SVKCVQPEK	9	HCV		LORF	2563	3,11		0.009	0.033		
1.0137	ITRAVESENK	9	HCV		LORF	2241	3,11		0.015	0.0079		
1.0957	CITSLSLGR	9	HCV		LORF	1042	3,11		0.0095	0.011		
1.0496	CVAGALVAK	10	HCV		LORF	1858	3,11		0.67	1.1		
1.0490	HLKHPFTGCK	10	HCV		LORF	1227	3,11		0.57	0.051		
1.052	RMVVGGEVHRL	10	HCV		NS1/ENV2	632	3,11		0.27	0.012		
1.0485	HURCHSKK	10	HCV		LORF	1390	3,11		0.27	0.025		
1.0484	TLGRCATVASK	10	HCV		LORF	1261	3,11		0.17	0.13		
1.1057	CVGMLPVR	10	HCV		LORF	3002	3,11		0.0029	0.002		
1.1063	LLFLLIADAR	10	HCV		NS1/ENV2	723	3,11		0.015	0		

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0014	FRDVVDFY	9	HIV		GAG	298	—	0.090				
2.0129	IVQYMDLY	9	HIV		GAG	875	—	0.064				
1.0028	TVLVDVGDAY	9	HIV		POL	802	—	0.018	<0.0002	0.0056		
1.0612	TVLVDVGDAY	10	HIV		POL	801	—	0.28	0	0.0004		
1.0615	VIQQTMDLY	10	HIV		POL	874	—	0.25	0.0007	0.0080		
2.0252	TVLVDVGDAY	10	HIV		POL	801	—	0.088				
1.0631	EVNNTDQY	10	HIV		POL	1187	—	0.053				
1.0641	LVVAVHVASY	10	HIV		POL	1229	—	0.039				
1.0642	PATTCQETAY	10	HIV		POL	1345	—	0.013				
2.0251	ESKQGPENPV	10	HIV		POL	742	1	0.013				
2.0255	QMAVFRHNFK	10	HIV		POL	1431	3		0.61	0.64		
2.0064	RYLKDQGQL	9	HIV		POL	2778	24			0.76		
2.0134	TVQMDQEP	9	HIV		POL	1033	24			0.30		
2.0131	TVQMDQEP	9	HIV		POL	1033	24			0.20		
2.0063	IVQEPFKNL	9	HIV		POL	1034	24			0.052		
2.0132	IVQEPFKNL	9	HIV		POL	1036	24			0.033		
2.0065	IVQYMDLY	9	HIV		POL	875	24			0.013		
2.0247	IVKWWILGL	10	HIV		POL	266	24			0.017		
2.0190	IVKWWILGL	10	HIV		POL	266	24			0.014		
2.0249	LYPLASLSEL	10	HIV		POL	506	24			0.014		
1.0049	KLACRHPYK	9	HIV		POL	1358	3,11	2.7	0.069			
1.0944	AVFHDFPK	9	HIV		POL	1434	3,11	0.17	1.8			
1.0032	AIRPSSMTK	9	HIV		POL	853	3,11	1.1	0.06			
1.0046	IVWGSTPK	9	HIV		POL	1075	3,11	0.085	0.37			
1.0079	KLTDERWNK	9	HIV		POL	1712	3,11	0.013	0.27			
1.0077	GIPAPAGLX	9	HIV		POL	788	3,11		0.23	0.065		
1.0059	QIEQLQLK	9	HIV		POL	1215	3,11		0.091	0.16		
1.0539	KIWPFSKGR	9	HIV		GAG	443	3,11		0.12	0.006		
1.0072	IAATDKQT	9	HIV		POL	1458	3,11		0.025	0.098		
1.0056	MOVELHPDK	9	HIV		POL	925	3,11		0.064	0.06		
1.0062	YLAWVPAHK	9	HIV		POL	1227	3,11		0.077	0.057		
1.0538	KIWPFSKGR	9	HIV		GAG	443	3,11		0.077	<0.0005		
1.0047	FVNTPLFLVK	9	HIV		POL	1111	3,11		0.012	0.066		
1.0024	NTPVFAIKK	9	HIV		POL	752	3,11		0.033	0.060		
1.0080	TVOCTHGIK	9	HIV		ENV	2421	3,11		0.0021	0.046		
1.0013	ILDIRQGPK	9	HIV		GAG	267	3,11		0.042	0.0048		

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0015	RDYVVDIPEVK	9	HTV		GAG	209	3.11	...	0.007	0.040
1.0058	GIQQAQDQDK	9	HTV		POL	1199	3.11	...	<0.0005	0.040
1.0064	VLFIDGIDK	9	HTV		POL	1234	3.11	...	0.038	0.032
1.0068	LVDIIDLNLK	9	HTV		POL	769	3.11	...	0.011	0.130
1.0073	TVVPRRKK	9	HTV		POL	1513	3.11	...	0.029	0.0039
1.0078	MTKILEPFR	9	HTV		POL	859	3.11	...	<0.0008	0.016
1.0083	TVVYGVVWIK	10	HTV		ENV	2185	3.11	...	3.8	7.8
1.0018	TVQPVILPEK	10	HTV		POL	935	3.11	...	0.16	5.6
1.0047	AVFHHNFKRK	10	HTV		POL	1434	3.11	...	0.66	0.05
1.0037	KVLFUDGIDK	10	HTV		POL	1253	3.11	...	0.36	0.78
1.0008	KLVDFREELNK	10	HTV		POL	768	3.11	...	0.51	0.090
1.0060	KLKFGMDGPK	10	HTV		POL	705	3.11	...	0.39	0.076
1.0095	FLGCKIWPSTK	10	HTV		GAG	440	3.11	...	0.32	0.024
1.1065	KIKNFVYTR	10	HTV		POL	1474	3.11	...	0.032	0.21
1.0010	GHPHPAGLKK	10	HTV		POL	768	3.11	...	0.011	0.17
1.0026	LVKLWVQLEK	10	HTV		POL	1117	3.11	...	0.055	0.082
1.0398	MGIGGCGFRK	10	HTV		POL	642	3.11	...	0.0099	0.053
1.0013	MTKILEPFRK	10	HTV		POL	859	3.11	...	0.013	0.039
1.0050	WVQDQNSDIK	10	HTV		POL	1504	3.11	...	<0.0005	0.021
1.0394	FLGCKIWPRIK	10	HTV		GAG	440	3.11	...	0.020	0.0013
1.1059	IVQOQNNLLR	10	HTV		ENV	2741	3.11	...	0.0024	0.019
1.0017	FTPDKKQHOK	10	HTV		POL	909	3.11	...	<0.0002	0.015
1.0005	LVEIETEMEK	10	HTV		POL	729	3.11	...	0.0002	0.012
1.0392	LVQVANPDK	10	HTV		GAG	327	3.11	...	<0.0002	0.011

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2.1	A3.2	A11	A24
1.0225	ISERYNRY	9	HPV	16	E6	80	1	7.8		0.0011	0.036	
1.0230	QAEPRDRAY	9	HPV	16	E7	44	1	0.021		<0.0002	<0.0002	
1.0610	LQDQEETCVY	10	HPV	18	E6	25	1	0.25		0.0056	0.012	
2.0159	TEKISERYRY	10	HPV	16	E6	77	1	0.17		<0.0009	0	
2.0162	YSKISERYRY	10	HPV	16	E6	77	1	0.11		<0.0009	0	
1.0599	HCDPDTLHY	10	HPV	16	E7	2	1	0.087		<0.0002	<0.0002	
1.0601	QPFDTDLY	10	HPV	16	E7	16	1	0.033				
1.0913	IIIDILECVY	10	HPV	16	E6	30	1	0.032				
1.0594	AVCDKCLFV	10	HPV	16	E6	68	1	0.095		0.0052	0.019	
2.0160	YSEIRELRY	10	HPV	18	E5	72	1	0.018		<0.0002	<0.0002	
2.0164	YSEIRELHY	10	HPV	18	E6	72	1	0.012				
2.0161	LLIICLRCQK	10	HPV	18	E6	101	3			0.061	0.070	
2.0032	HTMLCQCK	9	HPV	18	E7	59	11			0.020	0.079	
2.0029	VIICKTYL	9	HPV	18	E6	33	24					0.30
2.0007	CRASYGTL	9	HPV	16	E6	67	24					0.057
2.0024	YTRDAPRDL	9	HPV	16	E5	49	24					0.032
2.0001	LTMNLRL	9	HPV	18	E5	98	24					0.019
2.0000	VIICDTELK	9	HPV	18	E6	85	24					0.010
1.0239	SYTCOTLK	9	HPV	18	E6	84	3,11			0.39	2.3	
1.0243	SYTCOTLK	9	HPV	18	E6	84	3,11			0.35	1.1	
1.0244	SYTCOTLK	9	HPV	18	E6	84	3,11			0.70	0.95	
1.0226	TELEBQDQK	9	HPV	16	E6	93	3,11			0.010	0.67	
1.0241	SIPPHACHK	9	HPV	18	E6	59	3,11			0.004	0.25	
1.0227	SIPPHACH	9	HPV	18	E6	59	3,11			0.017	0.12	
1.0223	IVCPMSQK	9	HPV	16	E7	89	3,11			0.035	0.023	
1.0997	KLKHLNEKR	9	HPV	18	E6	117	3,11			0.025	<0.0005	
1.0234	LLRCLRCQK	9	HPV	18	E6	102	3,11			0.019	0.0012	
1.0653	ILLICLRCQK	9	HPV	16	E6	33	3,11			0.0016	0.019	
1.0999	CIDPSKIR	9	HPV	18	E6	68	3,11			0.07	0.0018	
1.0998	CIDPSKIR	9	HPV	18	E6	68	3,11			0.010	0.0009	
1.0596	GTMLCQYK	10	HPV	16	E6	92	3,11			0.010	0.98	
1.0606	LLIICLRCQK	10	HPV	18	E6	101	3,11			0.076	0.29	
1.0598	LLIICLRCQK	10	HPV	16	E6	106	3,11			0.12	0.24	
1.0639	LLIICLRCQK	10	HPV	18	E6	101	3,11			0.16	0.11	
1.0614	LTEVFEPAK	10	HPV	18	E6	41	3,11			0.0009	0.11	
1.0625	GYCPGQSK	10	HPV	16	E7	88	3,11			0.015	0.040	
1.0625	LTEVFEPAK	10	HPV	18	E6	41	3,11			0.012	0.041	
1.0591	DLILBCVYK	10	HPV	16	E6	32	3,11			0.0065	0.021	
1.1101	KLKHLNEKR	10	HPV	18	E6	117	3,11			0.013	0	
1.1095	CVYCKQOLR	10	HPV	16	E6	37	3,11			0.01	0.0059	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A21	A32	A41	A54
2.000	EVPPPPHL	9	MACE	3		101	1	18	0.0002	0.0009	0	0
3.017	EADPPTTY	9	MACE	5/51		161	1	69	0.0006	0.0006	0	0
1.0258	TOOLVREK	9	MACE	1		269	1	21	0	0.0002	0	0
3.0173	EVPPGTVY	9	MACE	6		161	1	19	0.0002	0.0002	0	0
1.0254	RAADPTGSHY	9	MACE	1		161	1	11	0	0	0	0
1.0259	IVPPKTVL	9	MACE	1		263	1	20	0.0013	0.005		
4.0053	TEPKVMEY	9	MACE	1		275	1	0.099				
2.0009	SELPPTTMY	9	MACE	3		9	1	0.055				
2.0011	GGVAGVWQY	9	MACE	3		77	1	0.050				
2.0008	SESPPTMY	9	MACE	2		9	1	0.043				
1.0253	MEVSKVY	9	MACE	1		128	1	0.011				
2.0012	ASPLFTMY	10	MACE	1		9	1	24	0.0009	0.003		
2.0017	LTQDQWQTY	10	MACE	1		239	1	12	0.0009	0.0023		
4.0114	EVSPVWVY	10	MACE	1		274	1	0.56				
2.0011	ASPLFTVY	10	MACE	3		9	1	67	0.0008	0.0024		
1.0249	EVWQVTEY	10	MACE	1		21	1	64	0.0007	0.0028		
4.0046	TEPVVPEY	9	MACE	1		275	3	0.71	0.0010			
4.0119	TTTPTFPR	9	MACE	1		66	1	12	0.0043	0.17		
4.0004	ALASDTEV	9	MACE	1		271	3	0.31	0.14			
4.0242	LTQDQWQK	9	MACE	1		239	1	0.003	0.0003	0.14		
4.0049	EVSPVWVY	9	MACE	1		274	1	0.002	0.0003	0.04		
4.0231	IVPPKTVL	9	MACE	1		263	1	0.002	0.0003	0.04		
4.0122	LEAVVTK	9	MACE	1		229	3	0.014	0.0009			
4.0224	EVSPVWV	10	MACE	1		97	3	0.011	0.0005			
4.0164	ADPLVTEK	10	MACE	1		293	3	0.13	0.0009			
4.0169	ESPLFVAK	10	MACE	1		107	1	0.35	0.27			
4.0118	EVPPVTEY	10	MACE	1		25	3	0.14	0.0008			
4.0120	IVPPKTVL	9	MACE	1		263	3	0.017	0.0007			
4.0119	EVSPVWV	10	MACE	1		274	1	0.019	0.0009			
4.0163	KAEMLSVK	10	MACE	1		125	3	0.15	0.0003	0.0007		
4.0125	EVSPVWV	10	MACE	1		270	11	0.18	0.024			
4.0070	STPLAVV	9	MACE	1		61	21					
2.0016	EVSPVWV	9	MACE	6		98	11	19	0.0009	0.13		
4.0127	TEPKVMEY	9	MACE	1		219	511					
1.1044	TTTPTFPR	9	MACE	1		66	511					
1.0257	LTQDQWQK	9	MACE	1		219	511					
1.0013	SLSAVV	10	MACE	1		96	511					
1.0047	LTQDQWQK	10	MACE	1		11	511					
1.0040	MEVSKVY	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1		11	511					
1.0040	EVSPVWV	10	MACE	1		11	511					
1.0044	EVSPVWV	10	MACE	1								

Pepptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A2,1	A3,2	A11	A24
1.0281	(SDC)TMLY	9	P53	-----	-----	225	1	29,5	-----	0,0010	0,029	-----
1.0287	GTAKSIVTCY	10	P53	-----	-----	117	1	0,33	0	0,023	0,049	0
1.0292	RVEGNLRLVEY	10	P53	-----	-----	196	1	0,022	-----	0,0014	0,0020	-----
1.0278	RVRAMATK	9	P53	-----	-----	156	3,11	-----	1,5	0,73	-----	-----
1.0276	CTYSPLALK	9	P53	-----	-----	124	3,11	-----	0,46	1,1	-----	-----
1.0285	NTSSSFQPK	9	P53	-----	-----	311	3,11	-----	0,0009	0,095	-----	-----
1.0284	RTEEDNLK	9	P53	-----	-----	283	3,11	-----	0,0015	0,091	-----	-----
1.0287	ELNEALELK	9	P53	-----	-----	343	3,11	-----	0,020	0,052	-----	-----
1.0278	RTEEDNLK	10	P53	-----	-----	283	3,11	-----	3,3	0,0080	-----	-----
1.1113	KTYQGSTYGR	10	P53	-----	-----	101	3,11	-----	2,6	0,88	-----	-----
1.1115	VRKRCRPHHER	10	P53	-----	-----	172	3,11	-----	0,099	0,0017	-----	-----
1.0269	NTSSSFQPK	10	P53	-----	-----	311	3,11	-----	0,0035	0,054	-----	-----
1.1121	RVCACFCGRDR	10	P53	-----	-----	273	3,11	-----	0,014	0,011	-----	-----
1.1116	GLAPRQHILR	10	P53	-----	-----	167	3,11	-----	0,013	0,0006	-----	-----

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Molif	A1	A2.1	A3.2	A11	A24
3.0175	KCEYFVEMY	9	PAP			322	1	3.4	<0.0002	0.0002	0	
3.0174	LCEYFIRKRY	9	PAP			81	1	0.78	<0.0002	0.0002	0	
3.0166	ASCHILTELY	9	PAP			311	1	0.77	<0.0002	<0.0002	0.055	0
3.0163	ESYKHNQVY	9	PAP			95	1	0.098	<0.0002	0.0002	0	
3.0237	LSEISSLSSLY	10	PAP			238	1	14	0.0026	0.0004	0	
3.0235	LSEISSLSSLY	10	PAP			238	1	12	0.0005	0.0004	0	
3.0236	LTOGLQMBQHY	10	PAP			70	1	0.62	0.0005	0.015	0.0024	0.0022
3.0238	KGETPVEEMY	10	PAP			322	1	0.018	0.0057	0.099		
3.0230	LVNEELNHMK	10	PAP			263	3		0.056	0.12		
3.0158	ATQDPSYK	9	PAP			274	11		0.10	1.2		
3.0221	ETLKSBERQK	10	PAP			170	11		<0.0004	0.014		
3.0161	LYFEKGEYF	9	PAP			318	24			2.5		
3.0160	LYCESVNDP	9	PAP			213	24			0.64		
3.0159	PYDDEATL	9	PAP			183	24			0.11		
3.0162	VNGLLPPY	9	PAP			302	24			0.032		
3.0232	PYASCHITEL	10	PAP			309	24			0.024		

Peptide#	Sequence	AA	Visns	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
1.0270	ALPDPFLY	9	PSA			223	1	0.011			
2.0337	VSGVWVFLY	10	PSA			65	1.11	0.15	-0.0003	0.0015	
1.0285	FLYOMSLK	9	PSA			65	1.11		0.34	0.057	
1.0273	VVWVTEKWK	9	PSA			243	1.11		0.0072	0.0033	
1.0272	YTKVWVHVK	9	PSA			229	1.11		0.0038	0.0046	
1.0269	SLLIONPLS	9	PSA			169	1.11		0.0024	0.007	
1.0260	IVGQWVCK	9	PSA			23	1.11		0.041	0.019	
1.0269	QVWVQKVTK	9	PSA			162	1.11		0.0086	0.014	
1.1112	SLYTKVWVHVK	10	PSA			227	1.11		0.35	0.23	
1.0263	LTAAMHCKNK	10	PSA			57	1.11		0.14	0.003	
1.0261	IVVGEVWCK	10	PSA			20	1.11		0.046	0.057	
1.0263	KVWVWVHVK	10	PSA			243	1.11		0.045	0.045	
1.1111	VTKVWVHVKAGE	10	PSA			169	1.11		0.0030	0.017	
3.0108	MILILSEPA	9	PSA			115	Random				

Table 5

Sequence	Size	Antigen	Strain	Molecule	Freq.	Pos.	Motif	A01	A03	A11	A24
								Bind.	Bind.	Bind.	Bind.
EDTPIGHLY	9	MAGE3a	3	analog		161	A01	12.5000			
AVDPIGHLY	9	MAGE3a	3	analog		161	A01	8.0000			
EVDPIGHLY	9	MAGE3a	3	analog		161	A01	5.5000			
FSPAFDNLY	10	HER-2/neu				1213	A01	5.5000	0.0005	0.0010	
EVDAIGHLY	9	MAGE3a	3	analog		161	A01	5.3500			
EVDPIGHLY	9	MAGE3a	3	analog		161	A01	5.0000			
EVDPGALY	9	MAGE3a	3	analog		161	A01	5.0000			
EVDPIGHAY	9	MAGE3a	3	analog		161	A01	4.6500			
EVDPIGHY	9	MAGE3a	3	analog		161	A01	3.4500			
EVDPGTHLY	9	MAGE3a	3	analog		161	A01	2.9500			
EVDPIGHSY	9	MAGE3a	3	analog		161	A01	2.6667			
EVDPASNTY	9	MAGE3a	3	analog		161	A01	2.4000			
EVDPGCHLY	9	MAGE3a	3	analog		161	A01	1.5000			
EVDPASNTY	9	HAGE	4			147	A01	1.2000	0.0005	0.0001	
PLSEDQQLY	9	PAP				2889	A01	0.8100	0.0002	0.0002	
LSAFSLHSLY	9	HCV				277	A01	0.5650			
IPSYKILIMY	10	PAP				310	A01	0.5467	0.0003	0.0002	
YASCHLTELX	10	PAP									
EVDPIGHLA	9	MAGE3a	3	analog		161	A01	0.3300			
CHOIAKGMXY	10	HER-2/neu				826	A01	0.2967	0.0003	0.0001	
VGSDCTTIIHY	10	p53				225	A01	0.2600	0.0003	0.0003	
EVAPIGHLY	9	MAGE3a	3	analog		161	A01	0.1800			

Table 5

Sequence	Size	Antigen	Strain	Molecule	Freq.	Pos.	Motif	A01	A03	A11	A24
ESMPNPFGRY	10	HER-2/neu						Bind.	Bind.	Bind.	Bind.
ASCVTACPY	9	HER-2/neu			280	A01	0.1800	0.0003	0.0003		
FSPAFDNLY	9	HER-2/neu			293	A01	0.0552	0.0008	0.0074		
ASPLDSTFY	9	HER-2/neu			1213	A01	0.0425	0.0002	0.0002		
RGIQLFENDY	10	HER-2/neu			997	A01	0.0290	0.0002	0.0004		
PASPLDSTFY	10	HER-2/neu			103	A01	0.0205	0.0003	0.0015		
PSQNTYQGSY	10	P53			996	A01	0.0148	0.0003	0.0001		
KSTRVPRAY	9	HCV			98	A01	0.0140	0.0003	0.0003		
DSSVULCECY	9	HCV			1236	A01	0.0134	0.0009	0.0001		
KISEYFRHICY	10	HPV	16	E6	79	A01	0.0090	0.0043	0.0038		
NLYVSLMLLY	10	HBV	adw	POL	20	1088	A01	0.0090			
GTRVRAHAIY	10	P53			154	A01/03	0.0027	0.0365	0.0002		
LTCGPADLMGY	11	HCV			126	A01/11	2.4500	0.0003	0.0120	0.0001	
YHACVGSPY	9	HER-2/neu			773	A01/A03	0.0400	0.0575	0.0079		
TLWAGILY	9	HBV	adr	POL	100	724	A03	0.0017	0.2667	0.0016	
KLNMASQIY	9	HIV		POL		958	A03	0.0070	0.1160	0.0006	
LYGFLILKY	9	MAGE1	1			109	A03	0.0033	0.0563	0.0012	
ILRGCTSFVY	9	HBV	adr	POL	80	1345	A03	0.0017	0.0440	0.0002	
RVZQGLPRT	10	HER-2/neu				545	A03	0.0015	0.0350	0.0050	

Table 5

Sequence	Size	Antigen	strain	Molecule	Freq	Pos.	Motif	A01	A03	A11	A24
QLVTLQMPY	9	HER-2/neu				795	A03	0.0024	0.0112	0.0039	
GLNKIVRMV	9	HIV		GAG		274	A03	0.0017	0.0103	0.0002	
LLQDNQVMPK	10	MAGE2	2			182	A03		0.0093	0.0014	
QVTDQAEHLK	10	HIV		POL		1419	A03		0.0089	0.0093	
LVSAGIRK	8	HIV	con			1246	A03		0.0091	0.0054	
VTRGRQK	8	HIV	con			1153	A03		0.0090	0.0065	
TVTDAAKLRG	11	HLA-Aw68 endogenous Peptide sequences				A03/11			0.1050	1.3000	
KTRGPIYKR	9	HLA-Aw68 endogenous Peptide sequences				A03/11			0.0340	0.8200	
SLTTKVVHY	9	PSA				237	A03/11	0.0017	0.6750	0.0140	
AVAAVARR	9	HLA-Aw68 endogenous Peptide sequences				A03/11			0.1600	0.0825	
KIQNPRVYY	9	HIV		POL		1474	A03/11	0.0056	0.1190	0.1350	
EMLESVAKYK	11	MAGE1				127	A03/11		0.0087	0.0099	
EVAPPPEVHRK	10	HLA-Aw68 endogenous Peptide sequences				A11			0.0008	0.0575	
ETAYFLLK	8	HIV	consensus			1351	A11		0.0037	0.0425	
RWGLLLALL	9	HER-2/neu				8	A24			1.2567	
PYVSRLG1	9	HER-2/neu				780	A24			0.1650	
VIMHIVVKCM	9	HER-2/neu				951	A24			0.1640	
AVSLTLQGL	9	HER-2/neu				440	A24			0.1250	
SYGVTWEL	9	HER-2/neu				907	A24			0.1200	
LYISAWPDSL	10	HER-2/neu				410	A24			0.0835	
VWSYGVTVW	9	HER-2/neu				905	A24			0.0800	

Table 5

Sequence	Size	Antigen	Strain	Molecule	Freq.	Pos.	Motif	A01	A03	A11	A24
								Bind.	Bind.	Bind.	Bind.
SYGGTYWELM	10	HER-2/neu				907	A24				0.0630
QYLAGLSTL	9	HCV				1777	A24				0.0475
TYLPTNDSL	9	HER-2/neu				63	A24				0.0375
EYLVSGFGWI	10	HBV		NUC	90	117	A24				0.0335
KFMLCAGRHW	9	PSA				190	A24				0.0305
WFHISCLTF	9	HBV		NUC	90	102	A24				0.0300
TYSTYGKFL	9	HCV				1296	A24				0.0225
YHIIHVKCM	10	HER-2/neu				951	A24				0.0218
RFRELVSEF	9	HER-2/neu				968	A24				0.0180
CYGLGMHEL	9	HER-2/neu				342	A24				0.0176
QYSPCQQRVRF	10	HCV				2614	A24				0.0175
KWHALESIL	9	HER-2/neu				887	A24				0.0149
EYLVPOQGFF	10	HER-2/neu				1022	A24				0.0120
RYSEDPTVPL	10	HER-2/neu				1111	A24				0.0117
RFTHQSDDW	9	HER-2/neu				898	A24				0.0107

Table 5

Sequence	AA	Mag	Strain	Mol.	Pos.	Notif	A1	A2.1	A3.2	A11	A24
DIVGFLLK	9	1			108	3,11			0.0040	0.0014	
QLYFGIDVK	9	1			152	3,11			0.0019	0.0051	
SLEQRSLHCK	10	1			2	3,11			0.015	0.015	
SLFRAVITRK	10	1			96	3,11			1.2	0.98	
DLVGFLLKX	10	1			108	1	0.0068		0.0069	0.0009	
MLESVIKNYK	10	1			128	3,11			0.14	0.027	
WEELSVMEVY	10	1			215	1	<0.0009		<0.0002	<0.0002	
VYDGREHSAV	10	1			223	1	<0.0009				
LUGGPJLLK	9	1			109	1	0.0033		0.056	0.0012	
LYTCGLGSX	9	1			171	1	0.0084		0.0014	<0.0002	
VLVTCGLGSX	10	1			170	1	0.0048	0	0.0013	0.007	
FLLKYRAR	9	1/2/3			112	3,11			0.0007	<0.0005	
PTTINFRQR	10	1			65	3,11			<0.0002	0.0033	
LNGFLLLKRY	10	1			109	3,11			0.0034	0.0023	
ENKLEYGRCR	10	1			246	3,11			<0.0002	0	
ELVHFLLK	9	2/3			108	3			0.0045	0.0011	
AYGEPRCLL	9	1			231	24				0.0007	
SYVLVTCGL	10	1			168	24			0.0006	0.0051	
EVVPISHLY	9	2			161	1	0.0028		<0.0002	<0.0002	
EVVRIGHLY	9	21			161	1	0.0002				
EVDPASNTY	9	4			161	1	0.0005				
EDAPTSNTY	9	5/51			161	1	9.9		0.0006	0.0006	0

Table 5

Sequence	AA	Wage	Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
EVDPIGHVY	9	6			161	1	1.9		<0.0002	<0.0002	0
EHLESVIK	9	1			127	3			<0.0003	0	
LVFGIDVK	9	1			153	3			0.0035	0.0037	
GVQGPSLK	9	1			266	3			<0.0003	0.0063	
VHEVYDGR	8	1			220	3			<0.0003	0.0007	
QEQKYLEY	8	1			244	1	0.0018				
NYGEPRKL	8	1			231	24					0.0017
VKEADPFGHSX	11	1			159	1	<0.0003				
IMEELSVMEVY	11	1			214	1	<0.0003				
EHLESVIKNYK	11	1			127	3	0.0087	0.0099			
EADPTISHTY	9	analog			161	1	0.68				
EVDPTISNTY	9	analog			161	1	1.8				
EALRAGQEA	9	1			14	2.1	0	<0.0002	0		
HSLEQRSIH	9	1			1	3		0.0025	0.0003		
QSPQGASAF	9	1			56	3		0.0004	0		
SAPPTTINF	9	1			62	3		<0.0003	0	0.0003	
TSCILESIF	9	1			90	3		<0.0003	0		
SCILESIFR	9	1			91	3		<0.0003	0.0026		
LPRAVITKK	9	1			97	3		0.011	0.0005		
VGFLLLKVR	9	1			110	3		0.0044	0.0051		
ESVIKVKHH	9	1			130	3		<0.0003	0		
VIKVKHKCF	9	1			132	3		<0.0003	0		

Table 5

Sequence	AA strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
ASESTQLVP	9	1,2	147	3			<0.0003	0	
LGDNQTMVK	9	1	183	3			0.0007	0.0048	
VHIAAMEGGH	9	1	200	3			<0.0003	0	
YDGREHFSAY	9	1	224	3			<0.0003	0	
LFDQDLVQEK	9	1	239	3			<0.0003	0.14	
CGVQGQPSLK	9	1	265	3			<0.0003	0.0037	
EMLESVIKNY	10	1	127	1	0.0006		<0.0002	<0.0002	0
KEADPTGHSY	10	-1	160	1	<0.0005		<0.0002	<0.0002	
ASAFPTTINF	10	1	61	3			<0.0003	<0.0002	
APPTTINPTR	10	1	63	3			<0.0003	0.0003	
PTTINPTRQR	10	1	65	3			<0.0003	0.0002	
STSCILESFL	10	1	89	3			<0.0003	<0.0002	
GFLLLKRYAR	10	1	111	3			0.0019	0.0008	
KAEMLESVIK	10	1	125	3			<0.0003	0.0097	
SVIKNYKHCP	10	1	131	3			<0.0003	<0.0002	
KASESQLQVP	10	1	146	3			<0.0003	<0.0002	0.0012
DVKEDADPTCH	10	1	158	3			<0.0003	<0.0002	
LYPHIAAMEGGH	10	1	199	3			0.0008	0.0005	
LSVMEVYDGR	10	1	218	3			<0.0003	0.012	
VMEVYDGREH	10	1	220	3			<0.0003	0.0002	0
YGRCRTVIPH	10	1	251	3			<0.0003	<0.0002	
SCCVQGQPSLK	10	1	264	3			0.0005	0.0089	

Table 5

Sequence	AA	Strain	Mag.	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
VPDSDPARY	9	1	new	254	1	0.0038					
QVPDSDPAPR	9	1	new	254	3		<0.0003	0.0002			
VIKVSARVR	9	1	new	284	3		0.0016	0			
PSLRERALR	9	1	new	296	3		<0.0003	0			
EFLNGPRL	9	1	new	264	24				0.0006		
ETSYVKVLEX	10	1	new	274	1	0.56					
LVQEKYLEIR	10	1	new	243	3		0.0008	0.0043			
QVPDSDPARY	10	1	new	254	3		0.0014	0.0003			
YVVKYLEVIK	10	1	new	277	3		0.0029	0.0015			
YVVIKVSARVR	10	1	new	283	3		0.019	0.0009			
RALAEETSYIK	10	1	new	270	11		0.18	0.24			
SYVKYLEVI	10	1	new	276	24				0.036		
FFPSLREALR	10	1	new	294	24					0.0044	
SVIKNYK	7	1 N	POL	131	3,11		0.0006	0.0028			
PVTKAEMLESVIK	13	1 n	E6	122	3,11		<0.0003	0			
ETSYVKYLEVIK	13	1 n	E6	273	3,11		0.0044	0.0003			
ITKKVADLVGFLIK	15	1 n	POL	102	3,11		0.40	1.0			
VTKAEMLESVIKNYK	15	1 n	POL	123	3,11		0.024	0.053			
VUGNWQYFFPVIFSK	15	3	POL	79	3,11		1.6	0.34			
PRALAETSY	9	1	new	268	1	<0.0018	<0.0003	<0.0002			
FATCGLISY	9	3		171	1	0.038	<0.0003	0.0004			
LEQRSIHK	9	1	new	3	3		<0.0002	0			

Table 5

Sequence	AA	Wage	Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
AELLESVYK	9	1		new	126	3			<0.0002	0.0011	
LESLVIK	9	1		new	129	3			<0.0002	0.0018	
EELSYMEVY	9	1		new	216	3			<0.0002	0	
MEYVDGREGH	9	1		new	221	3			<0.0002	0	
DSDPARYEF	9	1		new	256	3			<0.0002	0	
KVSVARVREF	9	1		new	285	3			0.0005	0	
VSVARVREFF	9	1		new	286	3			0.0003	0.0026	
HSPQGASSF	9	-2			56	3			<0.0002	0	
TTINYTLWR	9	2			66	3			0.089	1.1	
QEEGCPRMF	9	2			83	3			<0.0002	0	
MFPDLESEF	9	2			90	3			<0.0002	0	0.014
SFQAAISR	9	2			96	3			<0.0002	0.0001	
EFAQAAISR	9	2			97	3			<0.0002	0.0002	
LVHFLLLKY	9	2,3			109	3			0.043	0.010	
AELLESVLR	9	2			126	3			<0.0002	0	
SVLRNCQDF	9	2			131	3			<0.0002	0	
VLRNCQDF	9	2			132	3			<0.0002	0	
DFFPVITSK	9	2			138	3			<0.0002	0.0022	
VITSKASEY	9	2			142	3			0.081	0.033	
VVEVVPISH	9	2			159	3			0.0007	0.010	
LGDNQVHPK	9	2			183	3			<0.0002	0.0061	
EODCAPEEK	9	2,3			205	3			<0.0002	0	

Table 5

Sequence	Wage	AA	Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
QEEEGCPSTR	9	3			83	3			<0.0002	0	
TFPDLESEF	9	3			90	3			<0.0002	0	0.0049
SEFQALSLR	9	3			96	3			<0.0002	0	
EFOQALSRK	9	3			97	3			<0.0002	0.0001	
SVVGNWQYF	9	3			131	3			<0.0002	0	
VIGGNWQYF	9	3			132	3			0.0022	0.0021	
YFFFVIFSK	9	3			138	3			0.0020	0.027	
ASSSLQAVF	9	3			147	3			0.0011	0.0089	
LAEVDPIGH	9	3			159	3			<0.0002	0	
IVLALIAR	9	3			196	3			0.0069	0.0011	
VQEKVILYR	9	1			244	11			<0.0002	0	
SHQEZEQPR	9	2			81	11			<0.0002	0	
NYKHCPEI	9	1	new		135	24					4.8
IPGTAESL	9	1	new		143	24					0.0013
GRLLIVLW	9	1	new		193	24					<0.0002
IPSKASEYL	9	2			143	24					0.023
EYIQLVFGI	9	2			149	24					3.5
MHQYTPPPVII	9	3			135	24					0.53
IPSKASSL	9	3			143	24					0.016
LGSVVGNWQY	10	3			129	1			<0.0003	0.0012	
IPATCLGLSY	10	3			170	1			0.0005	0.0004	
TSCILESILFR	10	1	new		90	3			<0.0002	0.015	

Table 5

Sequence	AA	Mag _{strain}	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
LESVIKNYKH	10	1	new	129	3		<0.0002	<0.0002	<0.0002	
REHSAYGEPA	10	1	new	227	3		<0.0002	<0.0002	<0.0002	
PDSDPARYEF	10	1	new	255	3		<0.0002	<0.0002	<0.0002	
LEVVIKYSAR	10	1	new	280	3		<0.0002	<0.0002	<0.0002	
VIKVSARVRF	10	1	new	283	3		<0.0002	<0.0002	<0.0002	
KVSVARVFFF	10	1	new	285	3		0.00013	0.00020	0.00013	
STINYTLWR	10	2		65	3		0.0014	0.091	0.0014	
SSNQEEECPR	10	2		80	3		<0.0002	<0.0002	<0.0002	
RMPDLESEF	10	2		89	3		<0.0002	<0.0002	0.0016	
ESEFQAAISR	10	2		95	3		<0.0002	<0.0002	<0.0002	
SEFQAAISRK	10	2		96	3		0.0012	0.0028	0.0012	
ISRKMKVELVH	10	2		102	3		<0.0002	<0.0002	<0.0002	
VELVHFLLLK	10	2		107	3		0.0009	0.0003	0.0009	
ELVHFLLLKY	10	2,3		108	3		0.0066	0.0003	0.0066	
LVHFLLLKYR	10	2		109	3		0.026	0.0022	0.026	
HFLLLKYR	10	2,3		111	3		0.0014	0.0002	0.0014	
KAELHLESVLR	10	2		125	3		<0.0002	0.0009	<0.0002	
ESVLRNQDF	10	2		130	3		<0.0002	<0.0002	<0.0002	
SVLRNCQDF	10	2		131	3		<0.0002	<0.0002	<0.0002	
NCQDFFPVIF	10	2		135	3		<0.0002	<0.0002	<0.0002	
QDFFPVIFSK	10	2		137	3		<0.0002	0.0083	<0.0002	
PVIFSKASEY	10	2		141	3		0.016	0.0033	0.016	

Table 5

Sequence	AA	Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
KASEYLQLVF	10	2		146	3			<0.0002	<0.0002	0.0030
EVEVEVPISH	10	2		158	3			<0.0002	<0.0002	
VEVVPISHLY	10	2		160	3			<0.0002	<0.0002	
ILVTCIOLSY	10	2		170	3			0.0036	0.0002	
LLGDNQVAPK	10	2		182	3			0.0093	0.0014	
IEGDCAPEEK	10	2		204	3			<0.0002	<0.0002	
STPPDLESEF	10	3		89	3			<0.0002	<0.0002	
ESEFQALSR	10	3		95	3			<0.0002	<0.0002	
SEFQALSRK	10	3		96	3			0.0010	0.0010	
LSRKVAAELVH	10	3		102	3			<0.0002	<0.0002	
AELVHFLLLK	10	3		107	3			0.0008	<0.0002	
LVHFLLLKVR	10	3		109	3			0.040	0.0014	
GSVVGHNQXF	10	3		130	3			0.0020	0.0008	
SVVGHNQXF	10	3		131	3			0.0085	0.0067	
KASSSSLQLVF	10	3		146	3			0.0003	0.0008	0.0021
ELMEVDPIGH	10	3		158	3			<0.0003	<0.0002	
MEVDPIGHLY	10	3		160	3			0.0004	0.0004	
VDPIGHLYIF	10	3		162	3			<0.0003	<0.0002	
LIVLVAIAR	10	3		195	3			0.028	0.0021	
REGDCAPEEK	10	3		204	3			<0.0003	<0.0002	
RQSEGSSSR	10	1	new	74	11			0.0009	0.0009	
LQLVFGIDVK	10	1	new	151	11			0.0050	0.0018	

Table 5

Sequence	AA	Wage strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
RQVFDSDPAR	10	1	new	252	11			<0.0003	<0.0002	
MNYPLMSQSY	10	3	new	68	11			<0.0003	<0.0002	
GFLIVLVHVI	10	1	new	193	24				0.0008	
SFSTINNTL	10	2		63	24				0.015	
EFOQAIISRKH	10	2		97	24				<0.0002	
LYLIVTCIGL	10	2		168	24				0.014	
NPQYFFPVVIF	10	3		135	24				0.017	
AVDPIGHLY	9	3	analog	161	1	8.0				
EADPIGHLY	9	3	analog	161	1	3.5				
EVDPASHTY	9	4		161	1	1.5				
EDTPIGHLY	9	3	analog	161	1	13				
EVDPGTHLY	9	3	analog	161	1	3.0				
AADSPSPPH	9	2		55	A11					
VPISHLYIL	9	2		170	P1					
MPKTGLLII	9	2		196	P1					
SNLIEVYEGR	9	2				226	A11			
DSVTAHPRK	9	2				236	A11			
VFAHPRKLL	9	2				238	A24			
MQDLVQEMY	9	2				247	A01			
DPACYEFNW	9	2				265	P2			
FLWGPRLI	9	2				271	A02			
ALIETSYVK	9	2				277	A03/A11			

Table 5

Sequence	AA	Mag ^o	Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
TSYVKVHH	9	2			281		A11				
EPHISYPL	9	2			296		P1				
ISYPLHER	9	2			299		A03/A11				
YPLHLERBAL	9	2			301		P1				
EPYTKAENL	9	2/3			128		P1				
VPGSDPACY	9	2/3			261		P2				
EGCLEARGEA	9	3			14		A03				
GLCLEARGEAL	9	-3			15		A02				
EARGEALGL	9	3			17		A02				
ALGLVGQA	9	3			22		A02/A03				
GLVGQAQPA	9	3			24		A02/A03				
LVGAQAPAT	9	3			25		A02				
PATEEQEAA	9	3			31		A02/A03				
EAASSSSTL	9	3			37		A02				
AAASSSSSTLV	9	3			38		A02				
LVEVTLGEV	9	3			45		A02				
EVTLGEVPA	9	3			47		A02/A03				
VTLGEVPA	9	3			48		A02/A03				
LPPTMMYPL	9	3			71		P1				
POLESEFQAA	9	3			99		A03				
HPIILKRYA	9	3			118		A03				
FFPVVPSKA	9	3			146		A03				

Table 5

Sequence	AA	Wage	Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
DPICHLYIF	9	3			170	P2					
GDNQIMPKA	9	3			191	A03					
MPKAGLIIII	9	3			196	P1					
AGLLITIVLA	9	3			199	A03					
KIWEELSVL	9	3			220	A02					
SYLEVTPGR	9	3			226	A03/A11					
EDSILLAGDPK	9	3			235	A03/A11					
SILGDPKXL	9	-	3		237	A02					
ILGDPKLL	9	3			238	A02					
FLWGPRLAV	9	3			271	A02					
PRALVETSY	9	3			275	A01					
RALVETSYV	9	3			276	A02					
ALVETSYVK	9	3			277	A03/A11					
LVETSYVKV	9	3			278	A02					
YVKVLHHAV	9	3			283	A02					
KVLHHAVKI	9	3			285	A02					
MVKISGGPH	9	3			290	A03/A11					
ISGGPHISY	9	3			293	A01/A03/A11					
GPHISYPPL	9	3			296	P1					
YPLHEWVL	9	3			301	P1					
VPISHLYILV	10	2			170	P1					
MPKIGLIIIV	10	2			196	P1					

Table 5

Sequence	AA	Wage	Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
VFEGREDSTV	10	2			230	A24					
HPRKILMQL	10	2			241	P1					
LMQDLVQENY	10	2			246	A01					
EFILNGPRLI	10	2			270	A24					
GPRALIETSY	10	2			274	P2					
RALIETSYVK	10	2			276	A11					
SYVKVLHHTL	10	2			282	A24					
SYPPHLERAL	10	2			300	A24					
APERKIKWEL	10	2/3			216	P1					
PLPEPSOHCK	10	3			2	A03/A11					
HCKPEEGLEA	10	3			9	A03					
EARGEALGLV	10	3			17	A02					
RGEALGLVGA	10	3			19	A03					
EALGLVGRQA	10	3			21	A02/A03					
LGIVGQAPRA	10	3			23	A03					
GLVGAQAPAT	10	3			24	A02					
QAPATEEQEA	10	3			29	A02/A03					
EAASSSSSTLV	10	3			37	A02					
TLVEVTLGEV	10	3			44	A02					
EVTLGEVPA	10	3			47	A02/A03					
PPPPQSPQGA	10	3			59	A03					
LPPTMMNXPPLW	10	3			71	P2					

Table 5

Sequence	AA	Residue	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
PDLSESEPOA	10	3		99	A03					
YFFPVIPSKA	10	3		145	A03					
LGDNQIMPKA	10	3		190	A03					
HPKAGLLIV	10	3		196	P1					
EVFEGREDSI	10	3		229	A02					
EDSILGDPKK	10	3		235	A03/A11					
SILGDPKKLL	10	3		237	A02					
ILGDPKKLLT	10	3		238	A02					
GDPKKLITQH	10	3		240	A03/A11					
DPKKLITQHF	10	3		241	P2					
LTQHFVQENY	10	3		246	A01/A03/A11					
FVQENYLEYR	10	3		250	A03/A11					
ACYEFLMGPR	10	3		267	A03/A11					
GPRALVETSY	10	3		274	P2					
RALVETSYVK	10	3		276	A03/A11					
ALVETSYVK	10	3		277	A02					
LVETSYVKL	10	3		278	A02					
YVKVLHRDKV	10	3		283	A03/A11					
MYK1SGCPHI	10	3		290	A02					
K1SGCPHISY	10	3		292	A01					
SPPHSPOGA	9	2		60	P2A					
APATEEQEA	9	3		30	P2A					

Table 5

Sequence	AA	Residue	Pos.	Motif	A1	A2.1	A3.2	A11	A24
DPPGSPGAA	9	3	60	P2A					
APATEEQQA	10	2	30	P2A					
FPDLESEFQAA	10	2/3	98	P2A					
APATEEQAA	10	3	30	P2A					
DPIGHLYIFAA	10	3	170	P2A					
EDDPFHSY	9	1	161	1	0.56	0	0	0.0002	<0.0002
KVADLNGFLL	10	1	105	0.0005	0.041	0.0039	0.0030	0.0070	
ASSSLPTTINY	10	3	8	1	2.3			0.043	
TQDLVQEKY	9	1	240	1	0.57	0.0001	0	0	0
LVQEKYLEX	9	1	243	3	0.16	0	0.0016	0.0098	0
ILLWQPIPVA	9	3		<0.0007	1.4	0.0048	0.0048	0	
EVDPIGHLY	9	3		3.7			0.0022		
ASSSPTTINY	10	2	8	1	0.016	0	0.0016	0.0054	0
VTCIGLGSY	8	1	172	1	0.022	0	0.0001	0.0007	0
SSSLPTTINY	9	3	9	1	0.037	0	0.013	0.12	0
GSVVGGMQY	9	3	77	1	0.0059	0	0.0009	0.025	0
DLVQEKYLEX	10	1	new	242	3	0	0.0010	0	0
SSSPTTINY	9	2	9	1	0.016	0	0.0095	0.056	0
MLESVIKNT	9	1	128	1	0.0016	0.0002	0.0006	0	0
KMVELVHPL	9	2		<0.0007	0.13	0.0007	0	0.0043	
KMVELVHPL	10	2	105	<0.0008	0.071	0.0004	0.0001	0.0008	
LVVQIELMEV	10	3	0.0030	0.065	0.0007	0	0	0	

Table 5

Sequence	AA	Wage	Strain	Noi.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
SLFRAVITK	9	1		96	3,11	<0.0007	0.0001	3.9	2.6	0	
ADLVGFLIK	10	1		107	3	0.0012	0.0003	0.0081	0.022	0	
ESLFRAVITK	10	1		95	3	<0.0008	0	0.0090	0.0052	0	
MLESVTKYK	10	1			0		0	0.034	0.0045	0	
LYGFLILK	8	1		109	3	0.0029	0.0002	0.027	0.034	0	
TTINFFTRQR	9	1		66	3,11	0	0	0.051	0.40	0	
LIGDNDQIMPK	10	1/3		182	3,11	<0.0007	0.0001	0.022	0.016	0	
SVMEVYDGR	9	1		219	3,11	<0.0006	0	0.059	0.32	0	
HSAYGEPRK	9	1		229	3	0.0007	0	0.0070	0.0015	0	
LLTQDLVQEK	10	1		238	3,11	<0.0007	0	0.0014	0.011	0	
LTQDLVQEK	9	1		239	3,11	0.0011	0	0.0002	0.16	0	
NYKHCFFPEIF	10	1		135	24	0	0	0	0	0.26	
LYIPATCQL	10	3		115	24	<0.0007	0	0.0006	0	0.0035	
NYPLNSQSY	9	3		16	24	<0.0006	0	0	0.0001	0.016	
SYVLVTCL	6	1		168	24	0.0029	0.00025	0.0020	0.0002	0.0026	
ETSYVKLEY	10	1			0.075	0	0.0009	0.0004	0		
TSYVKLEY	9	1		275	3	0.082	0	0.23	0.013	0	
FLNGPRALA	9	1			<0.0006	0.027	0.0015	0	0		
ALAETSYVK	10	1		271		<0.0007	0.017	0.0011	0.0029	0	
RVRFPPSLR	10	1		290	3	<0.0007	0	0.25	0.0035	0	
ALAETSYVK	9	1			<0.0006	0.0002	0.17	0.39	0		
LTQDLVQEKY	10	1		239	1	0.041	0	0	0.0002	0	

Table 5

Sequence	AA	Wage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
GFLILKRYA	9	1						0.0004	0.0002	
CFPEITGKA	9	1						0	0	
FFFFPSLREAA	9	1						0	0	
FFFFPSLREAA	9	1						0	0	
HCFPEITGK	9	1		138	3,11			0.0017	0.0022	
RSLHICKPEEA	10	1						0.0001	0.0008	
EPLKMDPRAA	10	1						0	0	
RFFFFPSLREAA	10	1						0.0004	0	
FFFFPSLREAA	10	1						0	0	

Table 5

Sequence	Antigen	Strain	Molecule	Position	Motif	A1	A2	A3	A11	A24	Max. Binding
FSPAFDNLYY	c-EthB2			1213	A01	5.5000		0.0005	0.0010		5.5000
CMQIAKGMSY	c-EthB2			826	A01	0.2967		0.0003	0.0001		0.2967
ESMPNPEGRY	c-EthB2			280	A01	0.1800		0.0003	0.0003		0.1800
ASCVTACFY	c-EthB2			293	A01	0.0552		0.0008	0.0074		0.0552
FSPAFDNLY	c-EthB2			1213	A01	0.0425		0.0002	0.0012		0.0425
ASPLDSTFY	c-EthB2			997	A01	0.0290		0.0002	0.0004		0.0290
RGTQLFEDNY	c-EthB2			103	A01	0.0205		0.0003	0.0015		0.0205
PASPLDSTFY	c-EthB2			996	A01	0.0148		0.0003	0.0001		0.0148
LSAFSLHSY	ICV			2889	A01	0.8100		0.0002	0.0002		0.8100
KSTKVPAAY	ICV			1236	A01	0.0134		0.0009	0.0001		0.0134
DSSVLCECY	ICV			1513	A01	0.0110		0.0002	0.0003		0.0110
ETDPIGHLY	MAGE-3 ^a	3	analog	161	A01	12.5010					12.5010
AVDPIGHLY	MAGE-3 ^a	3	analog	161	A01	8.0000					8.0000
EVDPIAHLY	MAGE-3 ^a	3	analog	161	A01	5.5000					5.5000
EVDIAIGHLY	MAGE-3 ^a	3	analog	161	A01	5.1500					5.1500
EVDPIGALY	MAGE-3 ^a	3	analog	161	A01	5.0000					5.0000
EVDPIGHAY	MAGE-3 ^a	3	analog	161	A01	4.6500					4.6500
EADPIGHLY	MAGE-3 ^a	3	analog	161	A01	3.4500					3.4500
EVDPTGHLY	MAGE-3 ^a	3	analog	161	A01	2.9500					2.9500
EVDPIGHISY	MAGE-3 ^a	3	analog	161	A01	2.6667					2.6667
EVDPIGHLY	MAGE-3 ^a	3	analog	161	A01	2.4000					2.4000
EVDPIGHIA	MAGE-3 ^a	3	analog	161	A01	0.3300					0.3300
EVAPIGHLY	MAGE-3 ^a	3	analog	161	A01	0.1800					0.1800
EVDPASNTY	MAGE-4	4		161	A01	1.5000					1.5000
VGSIDCTT1HY	P53			225	A01	0.2600		0.0003	0.0003		0.2600
PSQRTYQGSY	P53			98	A01	0.0140		0.0003	0.0003		0.0140
PLSEDQOLLY	PAP			147	A01	1.2000		0.0005	0.0001		1.2000
IPSYKKLIMY	PAP			277	A01	0.5650					0.5650
YASCHLTELV	PAP			310	A01	0.5467		0.0003	0.0002		0.5467

Table 5

sequence	Antigen	Strain	Molecule	Position	Molff	A1	A2	A3	A11	A24	Max. Binding
					Binding	Binding	Binding	Binding	Binding	Binding	
RVLQCLPREY	c-ErbB2			545	A03	0.0015	0.0350	0.0050	0.0350
QLVTQLMPY	c-ErbB2			795	A03	0.0024	0.0112	0.0039	0.0112
VMAVGGSFY	c-ErbB2			773	A03	0.0400	0.0575	0.0079	0.0575
TLWKGAGILY	HIV	adr	POL	724	A03	0.0017	0.2667	0.0016	0.2667
ILRGTSFVY	HIV	adr	POL	1345	A03	0.0017	0.0440	0.0012	0.0440
KLWAQSIY	HIV		POL	958	A03	0.0070	0.1160	0.0016	0.1160
CLNKRIVRMY	HIV	MAGE-1	GAG	274	A03	0.0017	0.0103	0.0002	0.0103
IVGFLLKY	HIV	P53		109	A03	0.0033	0.0563	0.0012	0.0563
GTRVRAAIY	HIV		POL	154	A03	0.0027	0.0365	0.0002	0.0365
KIQNFRVYY	HIV		POL	1474	A03/A11	0.0056	0.1190	0.1350	0.1350
SLYTRKWHY	HIV	PSA		237	A03/A11	0.0017	0.6750	0.0140	0.6750
UTCGFAD1MGY	HIV			126	A1	2.4500	0.0003	0.0120	0.0001	...	2.4500
ETAYFLLK	HIV	con		1351	A11	0.0037	0.0425	0.0025	0.0425
RWGLLLALL	c-ErbB2			8	A24	1.2567
PYVSRLLG1	c-ErbB2			780	A24	0.1650
VYIMIVKCM	c-ErbB2			951	A24	0.1640
AYSIITLQGL	c-ErbB2			440	A24	0.1250
SYGVTWEL	c-ErbB2			907	A24	0.1200
I.YISAMPDSL	c-ErbB2			410	A24	0.0835
VWSYGVIVW	c-ErbB2			905	A24	0.0800
SYGVTWELM	c-ErbB2			907	A24	0.0630
TYLPTNASL	c-ErbB2			63	A24	0.0375
VYIMIVKCM	c-ErbB2			951	A24	0.0218
RFRELVSEF	c-ErbB2			968	A24	0.0180
CYGLGMELH	c-ErbB2			342	A24	0.0176
KMMALESIL	c-ErbB2			887	A24	0.0176
EYLVPOOGFF	c-ErbB2			1022	A24	0.0149
RYSEDPTVPL	c-ErbB2			1111	A24	0.0120
RFTIOSDVM	c-ErbB2			898	A24	0.0117
						0.0107

Table 5

Sequence	Antigen	Strain	Molecule	Position	Motif	A1	A2	A3	A11	A24	Max. Binding
EXLVSGGWVI	HBV		NUC	117	A24					0.0335	0.0335
WFIIISCLTF	HBV		NUC	102	A24					0.0300	0.0300
QYLAGLSTI	ICV			177	A24					0.0475	0.0475
TVSTYKGKFL	ICV			1296	A24					0.0225	0.0225
QYSPGQRVEF	ICV			2614	A24					0.0175	0.0175
KFMLCAGRW	PSA			1911	A24	0.0003				0.0305	0.0305

Table 6

AA	SEQUENCE	SOURCE
9	GLNKIVRMY	HIV GAG 274
9	KLNWASQIY	HIV POL 958
9	KIQNFRVYY	HIV POL 1474
9	TLWKAGILY	HBV adr POL 724
9	ILRGTSFVY	HBV adr POL 1345
9	SLYTAKVVHY	PSA 237
9	NTSSSPQPK	p53 311
9	NVKIPVAIK	c-ERB2 745
10	TLGFGAYMSK	HCV LORF 1261
10	GTRVVRAMAIY	p53 154
10	EAYSPVSTSK	HBV adw POL 887
9	QITKIQNFR	HIV POL 1471
9	NITGLILTR	HIV ENV 2633
9	FLWEWASVR	HBV adr ENV 324
9	RTPSPRRRR	HBV adr CORE 549
9	SLARGNQGR	HBV adr POL 805
10	VAYQATVCAR	HCV LORF 1587
10	KTYQGSGYGF	p53 101
9	WMCLRRFII	HBV ayw 237
9	WMCLRRFII	HBV ayw 237-245
9	KFMLCAGRW	PSA 190
10	IMPKTGFLII	MAGE 1 188
8	ETAYFLLK	HIV con 1351
11	LTCGFADIMGY	HCV 126
9	CSPHHTALR	HBV NUC:XNUCFUS 48
9	VMPKTGLI	MAGE 2 188
9	VMPKTGLI	MAGE2 188-196
9	VAELVHFLL	MAGE 3 106
9	IMPKAGLLI	MAGE 3 188
10	VMPKTGLII	MAGE 2 188
10	VMPKTGLII	MAGE2 188-197

AA	SEQUENCE	SOURCE
9	ASCVTACPY	c-ErbB2 293
9	VMAGVGSPY	c-ErbB2 773
9	ASPLDSTFY	c-ErbB2 997
9	FSPAFDNL	c-ErbB2 1213
9	KSTKVPAA	HCV 1236
9	DSSVLCECY	HCV 1513
9	LSAFSLHSY	HCV 2889
9	PLSEDQLLY	PAP 147
9	YAVCDKCLK	HPV 16 E6 67
9	CMSCCRSSR	HPV 16 E6 143
9	RWGLLLALL	c-ErbB2 8
9	TYLPTNASL	c-ErbB2 63
9	CYGLGMEL	c-ErbB2 342
9	AYSLLQGL	c-ErbB2 440
9	PYVSRLLGI	c-ErbB2 780
9	KWMALESIL	c-ErbB2 887
9	RFTHQSDVW	c-ErbB2 898
9	VWSYGVTVV	c-ErbB2 905
9	SYGVTVWEL	c-ErbB2 907
9	VYMIMVKCW	c-ErbB2 951
9	RFRELVSEF	c-ErbB2 968
9	WFHISCLTF	HBV NUC 102
9	TYSTYGFEL	HCV 1296
9	QYLAGLSTL	HCV 1777
10	IPSYKKLIMY	PAP 277
10	RGTQLFEDNY	c-ErbB2 103
10	ESMPNPEGRY	c-ErbB2 280
10	CMQIAKGMSY	c-ErbB2 826
10	PASPLDSTFY	c-ErbB2 996
10	FSPAFDNLYY	c-ErbB2 1213
10	PSQKTYQGSY	p53 98
10	VGSDCTTIHY	p53 225
10	YASCHLTEL	PAP 310
10	LYISAWPDSL	c-ErbB2 410

AA	SEQUENCE	SOURCE
10	SYGVTVWELM	c-ErbB2 907
10	VYMIMVKCWM	c-ErbB2 951
10	EYLVPQQGFF	c-ErbB2 1022
10	RYSEDPTVPL	c-ErbB2 1111
10	SYLVSFGVWI	HBV NUC 117
10	QYSPGQRVEF	HCV 2614
9	VYNFATCGI	LCMV glyco 35
9	GYCLTKWMI	LCMV glyco 283
9	MFEALPHII	LCMV glyco 7
9	IFALISFLL	LCMV glyco 43
9	LFKTTVNSL	LCMV glyco 342
9	LYTVKYPNL	LCMV nucleo 204
9	PYIACRTSI	LCMV nucleo 314
10	GYCLTKWMIL	LCMV glyco 283
10	AYLVSIFLHL	LCMV glyco 446
9	RWCIPWQRL	CEA 10
9	IYPNASLLI	CEA 101
9	LWWVNNQSL	CEA 177
9	LYGPDAPTI	CEA 234
9	VYAEPPKPF	CEA 318
9	LWWVNNQSL	CEA 355
9	LYGPDDPTI	CEA 412
9	TYYRPGVNL	CEA 425
9	LYGPDTPII	CEA 590
9	QYSWRINGI	CEA 624
9	TYACFVSNL	CEA 652
9	VWKTWGQYW	gp100 152
9	TWGQYWQFL	gp100 155
9	RYGSFSVTL	gp100 479
9	LMAVVVLASL	gp100 606
9	HWLRLPRIF	gp100 636
9	SYKHEQVYI	PAP 96
9	AMTNLAALF	PAP 116
9	VFLTLSVTW	PSA 2

AA	SEQUENCE	SOURCE
9	TWIGAAPLI	PSA 9
9	CYASGWGSI	PSA 148
10	YMIMVKCWMI	c-ErbB2 952
10	RWCIPWQRLL	CEA 10
10	FWNPPPTAKL	CEA 27
10	QYSWFVNGTF	CEA 268
10	TFQQSTQELF	CEA 276
10	VYAEPPKPF	CEA 318
10	YYRPGVNLSL	CEA 426
10	QYSWLIDGNI	CEA 446
10	SYLSGANLNL	CEA 604
10	HFLRNQPLTF	gp100 231
10	LFPPEGVSIW	PAP 123
10	TWIGAAPLIL	PSA 9
10	HYRKWIKDTI	PSA 244
9	KLRKPKHKK	<i>P. falciparum</i> CSP 104
9	KILSVFFLA	<i>P. falciparum</i> EXP-1 2
9	ALFFIIIFNK	<i>P. falciparum</i> EXP-1 10
9	GTGSGVSSK	<i>P. falciparum</i> EXP-1 28
9	VLYNTEKGR	<i>P. falciparum</i> EXP-1 99
9	KYKLATSVL	<i>P. falciparum</i> EXP-1 73
9	PSENERGYY	<i>P. falciparum</i> LSA1 1664
9	FLKENKLNK	<i>P. falciparum</i> LSA1 111
9	GVSENIFLK	<i>P. falciparum</i> LSA1 105
9	ILVNLLIFH	<i>P. falciparum</i> LSA1 12
9	KSLYDEHIK	<i>P. falciparum</i> LSA1 1854

AA	SEQUENCE	SOURCE
9	LLIFHINGK	<i>P. falciparum</i> LSA1 16
9	QSSLPQDNR	<i>P. falciparum</i> LSA1 1676
9	QTNFKSLLR	<i>P. falciparum</i> LSA1 94
9	RINEEKHEK	<i>P. falciparum</i> LSA1 49
9	SLYDEHIKK	<i>P. falciparum</i> LSA1 1855
9	VLAEDLYGR	<i>P. falciparum</i> LSA1 1647
9	VLSHNSYEK	<i>P. falciparum</i> LSA1 60
9	FYFILVNLL	<i>P. falciparum</i> LSA1 9
9	YYIPHQSSL	<i>P. falciparum</i> LSA1 1671
9	PSDGKCNLY	<i>P. falciparum</i> TRAP 207
9	LACAGLAYK	<i>P. falciparum</i> TRAP 511
9	LLACAGLAY	<i>P. falciparum</i> TRAP 510
9	LSTNLPYGR	<i>P. falciparum</i> TRAP 122
9	QGINVAFNR	<i>P. falciparum</i> TRAP 192
9	RGDNFAVEK	<i>P. falciparum</i> TRAP 307
9	RSRKREILH	<i>P. falciparum</i> TRAP 262
9	SLLSTNLPY	<i>P. falciparum</i> TRAP 120
9	KYLVIVFLI	<i>P. falciparum</i> TRAP 8
9	PYAGEPAPP	<i>P. falciparum</i> TRAP 528

AA	SEQUENCE	SOURCE
10	VTCGNGIQVR	<i>P. falciparum</i> CSP 375
10	GTGSGVSSKK	<i>P. falciparum</i> EXP-1 28
10	LALFFIIFNK	<i>P. falciparum</i> EXP-1 9
10	FQDEENIGIY	<i>P. falciparum</i> LSA1 1794
10	FILVNLLIFH	<i>P. falciparum</i> LSA1 11
10	HVLSHNSVEK	<i>P. falciparum</i> LSA1 59
10	KSLYDEHIKK	<i>P. falciparum</i> LSA1 1854
10	ALLACAGLAY	<i>P. falciparum</i> TRAP 509
10	IIRLHSASK	<i>P. falciparum</i> TRAP 100
10	LLACAGLAYK	<i>P. falciparum</i> TRAP 510
10	RLHSDASKNK	<i>P. falciparum</i> TRAP 102
9	ILGFVFTLT-NH2	Flu Matrix 59-67
10	KGILGFVFTL- NH2	Flu Matrix 57-66
9	KLQCVPLHV	PSA 166-174 P/D
9	KLQCVPLHV	PSA 166-174 P/D
9	KLQCVPLHV	PSA 166-174 P/D
11	KQVPLRPMTYK	940.03 N-terminal extension
9	KLYEIVAKV	A2.1 consensus
9	KLAEYVAKV	A2.1 consensus
9	KLAEVYKV	A2.1 consensus
9	KVFEYLINK	A3.2 consensus
10	KVFPYALINK	A3.2 consensus
9	AVFAYAAAK	A3.2 consensus
9	ALEPAIAKY	A1 consensus

AA	SEQUENCE	SOURCE
9	YLEPAIAKY	A1 consensus
9	ALEPYIAKY	A1 consensus
9	YLEQYIEKY	A1 consensus
9	GTEKLLAKY	A1 consensus
9	ATEPAIAKY	A1 consensus
9	ATNYPAIQK	A11 consensus
9	ATNVPAIQK	A11 consensus
9	ATNAPYIQK	A11 consensus
9	ATNAVYIQK	A11 consensus
9	ATNAAYAQK	A11 consensus
9	AVNAAYAQK	A11 consensus
9	AVNAPYIQK	A11 consensus
9	AVNAVYIQK	A11 consensus
9	PTDPKLINY	A1 consensus
9	GTDPKLINY	A1 consensus
9	YTDPKLINF	A1 consensus
9	FTDPKLINY	A1 consensus
9	FTDQAVIKY	A1 consensus
9	YTDQAVIKF	A1 consensus
9	YTDQKLINF	A1 consensus
9	STNPKPQKK	HCV-core 2-10
11	STNPKPQKKNK	HCV-core 2-12
9	SFFPEITYI	self peptide of P815 analog: Y2 to F,
9	ATDPNFLY	A1 consensus
9	ATDKNFLY	A1 consensus
9	ALMEKIYQV	A2.1 consensus peptide
9	ALSEKIYQV	A2.1 consensus peptide
9	AVYDPIIQQK	A3.2 consensus peptide
9	AVYDKIIQQK	A3.2 consensus peptide
9	AVMNPMPMIQK	A11 consensus peptide

AA	SEQUENCE	SOURCE
9	AVMNEMIQK	A11 consensus peptide
9	AYMDMVNSF	A24 consensus peptide
9	AYIDNVNSF	A24 consensus peptide
9	KLAAAAAAAK	A3.2/A11 poly-A analog
9	DVFRDPALK	Aw68 endogenous
9	GYKDGNEYI	Lm listeriolysin 91-99
10	MMWYWGPSLY	HBV
11	WMMWYWGPSLY	HBV
9	RYLRDQQLL	HIV env
8	FLLKYRA	MAGE-1
9	IMPKTGFLI	MAGE-1
9	VADLVGFLL	MAGE-1
10	IMPKTGFLII	MAGE-1
11	FLIIVLVMIAAM	MAGE-1
11	CILESCFRAVI	MAGE-1
9	MYRPDAIQL	P. Yoelii SSP2 143
10	NYSPNGNTNL	P. Yoelii SSP2 119
9	KFNPMKTHI	Kd consensus peptide
9	AMIKNLDFI	Db consensus
9	AMIKNLYFI	Db consensus analog
11	STLPETYVVRR	HCV 141-151 analog
9	QYDDAVYKL	Cw4 consensus
10	FQDPQERPRK	HPV16 E6
10	VFEFAFKDLF	HPV18 E6
9	VVYRDSIPH	HPV18 E6
9	IFEANGNLI	Flu HA 240-248
9	IYATVAGSL	HA 529-537

AA	SEQUENCE	SOURCE
9	SYIPSAEKI	P. bergaei CS 252-260
9	KYQAVTTTL	Tumour P198 14-22
10	MYPHFMPTNL	MCMV pp89 167-176
9	AYPNVSAKI	Lm listeriolysin 196-204
9	AYTGGKINI	Lm listeriolysin 413-421
9	SAISSL SK	HBV ENV 159
9	QAGFFLLTK	HBV ENV 190
9	SALYREALK	HBV NUC 64
9	RAKWNNTLK	HIV env 370
9	RATQIPSYK	PAP 273
9	TAAH CIRNK	PSA 58
9	MAVFIHNFK	HIV pol 909
9	TAGILELLK	HPV 6b E1 192
9	RAALLGKF	HPV 6b E1 205
9	CATMCRHYK	HPV 6b E1 406
9	TAAC SHEGK	Flu HA-1 132
9	NANANSAVK	P. fal csp 304
9	GAFK VPGVK	LCMV glyco 484
9	RARVHPTTR	HBV POL 244
9	CALPPTSAR	HBV X 69
9	NMLESILIK	LCMV nuc 259
9	WMILAAELK	LCMV glyco 289
9	EMNLPGRWK	HIV pol 107
9	SSLQSKHRK	HBV POL 201
9	GSTHVSWPK	HBV POL 398
9	TSDLEAYFK	HBV X NUC FUS 105
9	ASQIYAGIK	HIV pol 438
9	ASCDK CQLK	HIV pol 769
9	MSLAADLEK	LCMV nuc 100
9	VSSKNLMEK	Mel. tyro 25

AA	SEQUENCE	SOURCE
9	LSTNLPYGK	P. falciparum ssp2 122
9	STDHIPILY	A1 Nat. Processed
9	STAPPAHGV	Breast mucin 9-17
9	LMAVVLASL	gp100
9	WSQKRSFVY	gp100
9	PLDCVILYRY	gp100
10	PSSVGSRSEY	gp100
9	YTAVVPLVY	Hu J chain 102-110

Table 7

AA	SEQUENCE	SOURCE
8	LTELTYFEK	PAP 315
9	TISPSYTYY	CEA 419
9	GTGCNGWFY	HPV 16/18 E1 11
9	LTEMVQWAY	HPV 6b/11 E1 358
9	ITVNNNSGSY	CEA 289
9	CTGWMFMVEA	HPV 6b/11 E1 14
9	ATVQDLKRK	HPV 6b/11 E1 77
9	AVESEISPR	HPV 6b/11 E1 101
9	FLNSNMQAK	HPV 6b/11 E1 393
9	ITRQTVIEH	HPV 6b/11 E1 341
9	IVGPPDTGK	HPV 6b/11 E1 476
9	KLIEPLSLY	HPV 6b/11 E1 254
9	KLWLHGTPK	HPV 6b/11 E1 462
9	KMSIKQWIK	HPV 6b/11 E1 420
9	VVAGFGIHH	HPV 6b/11 E1 238
9	HLFGYSWYK	CEA 61
9	ISPSYTYYR	CEA 420
9	HTQVLFIAK	CEA 636
9	ITVYAEPPK	CEA 316
9	ITVSAELPK	CEA 494
9	RLQLSNGNR	CEA 190
9	RLQLSNGNR	CEA 546
9	RINGIPQHQ	CEA 628
9	SNMQAKYVK	HPV 6b/11 E1 396
9	EWITRQTVI	HPV 6b/11 E1 339
9	FPERLSSSL	HPV 6b/11 E1 613
9	NWKPTVQFL	HPV 6b/11 E1 439
10	PTISPSYTYY	CEA 418
10	PTISPLNTSY	CEA 240
10	HSASNPSPQY	CEA 616
10	KLIEPLSLYA	HPV 6b/11 E1 254
10	ATVGPPDTGK	HPV 6b/11 E1 475
10	DCATMCRHYK	HPV 6b/16 E1 405
10	KLWLHGTPKK	HPV 6b/11 E1 462
10	WVAGFGIHH	HPV 6b/11 E1 237

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AA	SEQUENCE	SOURCE
10	TITVSAELPK	CEA 493
10	TFWNPPITAK	CEA 26
10	TISPSYTYYR	CEA 419
10	TISPLNTSYR	CEA 241
10	RTLTLFNVTR	CEA 198
10	RTLTLFNVTR	CEA 554
10	RTLTLLSVTR	CEA 376
10	ATPGPAYSGR	CEA 89
10	ASGHSRTTVK	CEA 483
10	QFLRHQNIEF	HPV 6b/11 E1 445
10	TFTFPNPPPF	HPV 6b/11 E1 586
9	RVDCTPLMY	Prost.Ca PSM 463
9	LLSLYGIHK	Prost.Ca PAP 243
9	SIVLPFDCR	Prost.Ca PSM 590
9	KSLYESWTK	Prost.Ca PSM 491
9	SMKHPQEMK	Prost.Ca PSM 615
9	SLYESWTKK	Prost.Ca PSM 492
9	YSLVHNLT	Prost.Ca PSM 471
9	HLTELYFEK	Prost.Ca PAP 314
9	RATQIPSYK	Prost.Ca PAP 273
9	ASGRARYTK	Prost.Ca PSM 531
9	SLYGIHKQK	Prost.Ca PAP 245
9	RDYAVVLRK	Prost.Ca PSM 598
9	SSHDLMLLR	Prost.Ca PSA 113
9	GAAPLILSR	Prost.Ca PSA 12
9	KIVIARYGK	Prost.Ca PSM 199
9	RAAPLLLAR	Prost.Ca PAP 2
9	VVLRKYADK	Prost.Ca PSM 602
9	GLPDRPFYR	Prost.Ca PSM 680
9	WLDRSVLAK	Prost.Ca PAP 25
9	KVFRGNKVK	Prost.Ca PSM 207
9	IVRSPGTLK	Prost.Ca PSM 398
9	KIYSISMKH	Prost.Ca PSM 610
9	RSVLAKELK	Prost.Ca PAP 28
9	STNEVTRIY	Prost.Ca PSM 348
9	GFFLLGFLF	Prost.Ca PSM 31

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AA	SEQUENCE	SOURCE
9	LYSDPADYF	Prost.Ca PSM 227
9	KYADKIYSI	Prost.Ca PSM 606
9	NYARTEDFF	Prost.Ca PSM 178
9	AYINADSSI	Prost.Ca PSM 448
9	SASFCCGSPY	HBV POL 165
9	AFTFSPTYK	HBV POL 655
9	SVVRRAFFH	HBV POL 524
9	RWMCLRRFI	HBV ENV 236
9	SWLSSLVPF	HBV ENV 334
9	SWWTSLNFL	HBV ENV 197
9	PWTHKVGNF	HBV POL 51
9	SFCGSPYSW	HBV POL 167
10	NADSSIEGNY	Prost.Ca PSM 451
10	GLDSVELAHY	Prost.Ca PSM 104
10	RATQIPSYKK	Prost.Ca PAP 273
10	LGFLFGWFIK	Prost.Ca PSM 35
10	SSIEGNYTLR	Prost.Ca PSM 454
10	KSLYESWTKK	Prost.Ca PSM 491
10	SLLSLYGIHK	Prost.Ca PAP 242
10	FLYNFTQIPH	Prost.Ca PSM 73
10	VIYAPSSHNK	Prost.Ca PSM 690
10	AVVLRKYADK	Prost.Ca PSM 601
10	KSPDEGFEGK	Prost.Ca PSM 482
10	IVRSFGTLKK	Prost.Ca PSM 398
10	RIYNVIGTLR	Prost.Ca PSM 354
10	LSLYGIHKQK	Prost.Ca PAP 244
10	MSLLKNRPLR	Prost.Ca PSA 99
10	ISMKHPQEMK	Prost.Ca PSM 614
10	RAVCGGVLVH	Prost.Ca PSA 43
10	GSAPPDSSWR	Prost.Ca PSM 311
10	SIPVHPIGYY	Prost.Ca PSM 291
10	CSGKIVIARY	Prost.Ca PSM 196
10	ETYELVEKFY	Prost.Ca PSM 557
10	RLLQERGVAY	Prost.Ca PSM 440
10	FYDPMFKYHL	Prost.Ca PSM 565
10	TYSVSFDSL	Prost.Ca PSM 624

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AA	SEQUENCE	SOURCE
10	LYNFTQIPHL	Prost.Ca PSM 74
10	GWRPRRTILF	Prost.Ca PSM 409
10	FAAPFTQCGY	HBV POL 631
10	RWMCLRRFII	HBV ENV 236
10	WFVGLSPTVW	HBV ENV 345
10	SWPKFAVPNL	HBV POL 392
10	VFADATPTGW	HBV POL 686
9	FIFHKFQTK	HTLV-I tax 276
9	FLTNVPYKR	HTLV-I tax 182
9	ITWDPIDGR	HTLV-I tax 54
9	SALQFLIPR	HTLV-I tax 66
9	LSFPDPGLR	HTLV-I tax 131
9	QSSSFIFHK	HTLV-I tax 272
9	GLCSARLHR	HTLV-I tax 34
9	RLPSFPTQR	HTLV-I tax 74
9	AMRKYSPFR	HTLV-I tax 108
9	ISGGLCSR	HTLV-I tax 31
9	ALFTAQEAK	HPV 16 E1 69
9	ATMCRHYKR	HPV 16 E1 406
9	FMSFLALK	HPV 16 E1 453
9	GVSFSELVR	HPV 16 E1 216
9	KAAMLAKFK	HPV 16 E1 204
9	LTNILNVLK	HPV 16 E1 191
9	LVRPFKSNK	HPV 16 E1 222
9	MSFLTALKR	HPV 16 E1 454
9	NSNASAFLK	HPV 16 E1 386
9	QMSMSQWIK	HPV 16 E1 419
9	RLKAICIEK	HPV 16 E1 109
9	SLFGMSLMK	HPV 16 E1 484
9	SMSQWIKYR	HPV 16 E1 421
9	TAAALYWYK	HPV 16 E1 315
9	VVILLVRYK	HPV 16 E1 274
9	ALLRYKCGK	HPV 18 E1 284
9	ATMCKHYRR	HPV 18 E1 413
9	CATMCKHYR	HPV 18 E1 412
9	FITFLGALK	HPV 18 E1 460

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AA	SEQUENCE	SOURCE
9	GVLILALLR	HPV 18 E1 279
9	KLRAQGNHR	HPV 18 E1 647
9	LILALLRYK	HPV 18 E1 281
9	LTTNIHPAK	HPV 18 E1 571
9	NMSQWIRFR	HPV 18 E1 428
9	NSNAAFLK	HPV 18 E1 393
9	SVAALYWYR	HPV 18 E1 322
9	WTYFDITYMR	HPV 18 E1 536
9	YVQAIVDKK	HPV 18 E1 19
9	IIKNFDIPK	GCDFP-15 36
9	VLAQVTELK	GCDFP-15 55
10	IIIKNFDIPK	GCDFP-15 35
10	TACLCDDNPK	GCDFP-15 87
10	AVLAVQTELK	GCDFP-15 54
10	TFYWDIFYTNR	GCDFP-15 97
9	ASCHLTLY	PAP 311
10	KGEYFVEMYY	PAP 322
10	LTAAHCIRNK	PSA 57
9	PLYDMSLLK	PSA 95
9	QVHPQKVTK	PSA 182
9	SLLKNRFLR	PSA 100
9	YTKVVHYRK	PSA 239
9	TLWKAGILY	HBV pol 150
9	SLYTKVVHY	PSA 237
9	PVNRPIDWK	HBV POL 612
9	RHYLHTLWK	HBV POL 719
11	HTLWKAGILYK	HBV POL 149
11	GTDNSVVLRSK	HBV POL 735
11	RVTGGVFLVDK	HBV POL 357
8	ATQIPSYK	PAP 274
9	WMNSTGFTK	HCV consensus
9	RVLEDGVNY	HCV consensus
9	RLLAPITAY	HCV consensus
9	GVLAALAAAY	HCV consensus
9	RVCEKMLAY	HCV consensus

TABLE 8

PEPTIDE	AA	SEQUENCE
1235.01	10	AVFDRKSDAK
26.0149	9	CALRFTSAR
26.0153	9	SSAGPCALR
F104.02	9	SLTPPHSAK
F105.01	9	AIFQSSMTK
F105.02	9	GIFQSSMTK
F105.03	9	AAFQSSMTK
F105.04	9	AIAQSSMTK
F105.05	9	AIFASSMTK
F105.06	9	AIFQASMTK
F105.07	9	AIFQSAMTK
F105.08	9	AIFQSSATK
F105.09	9	AIFQSSMAK
F105.10	9	AIFQSSMTA
F105.11	9	FIFQSSMTK
F105.12	9	SIFQSSMTK
F105.14	9	ANFQSSMTK
F105.16	9	AIFQCSMTK
F105.17	9	AIFQSSMTR
F105.19	9	AIFQSSMTY
F105.20	9	AIQSSMTR
F105.21	9	AIFQRSMTR
F105.24	10	PAIFQSSMTK
F105.25	10	AIFQSSMTKI
27.0103	9	AIIILHQQQK
27.0104	9	YGFRRLGFLH
27.0108	9	SSCMGGMNR
27.0235	10	TCTYSPALNK
27.0239	10	NSSCMGGMNR
27.0240	10	SSCMGGMNRR
27.0250	10	KSKKGQSTS
27.0252	10	TSRHKKLMFK
28.0062	8	FMFSPTYK
28.0063	8	FVFSPTYK
28.0066	8	TMLXMXKK

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PEPTIDE	AA	SEQUENCE
28.0322	9	SMICSVVRR
28.0323	9	SVICSVVRR
28.0324	9	KVGNFTGLK
28.0325	9	KVGNFTGLR
28.0326	9	VVFSSQFSR
28.0327	9	SVNRPIDWK
28.0328	9	TLWKAGILK
28.0329	9	TLWKAGILR
28.0330	9	TMWKAGILY
28.0331	9	TVWKAGILY
28.0332	9	RMYLHTLWK
28.0333	9	RVYLHTLWK
28.0334	9	AMTESPTYK
28.0335	9	AVTFSPTYK
28.0336	9	SVVRRAFPR
28.0337	9	SVVRRAFPK
28.0338	9	ISEYRHYYX
28.0339	9	GTGXNGWFY
28.0340	9	ASXHLTELY
28.0341	9	ASXDKXQLK
28.0371	9	RVXEKMAKY
28.0372	9	XTGWFMVYA
28.0374	9	HISXLTGFR
28.0375	9	AVXTRGVAK
28.0377	9	HIIIPXHSKK
28.0378	9	HTMLLXMXKK
28.0381	9	RLKAIXIEK
28.0383	9	TLFXASDAK
28.0384	9	ALLRYKXKGK
28.0387	9	ATMXRHYKR
28.0388	9	XATMXRHYK
28.0390	9	ATMXKHYRR
28.0391	9	LLAXAGLAY
28.0392	9	LAXAGLAYK
28.0393	9	SIVLPFDXR
28.0394	9	AAXWWAGIK
28.0628	10	QMFIFSPYK

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PEPTIDE	AA	SEQUENCE
28.0629	10	QVFTPSPTYK
28.0630	10	TMWKAGILYK
28.0631	10	TVWKAGILYK
28.0632	10	VMGGVFLVDK
28.0633	10	VVGGVFLVDK
28.0635	10	SVLPETTVVR
28.0638	10	HTLWKAGILK
28.0640	10	HMLWKAGILY
28.0395	9	SADKSVVRR
28.0644	10	GTFNSVVLSR
28.0645	10	YMFDVVLGAK
28.0646	10	MMWYWGPSLK
28.0647	10	MMWYWGPSLR
28.0665	10	IVGGWEXEK
28.0667	10	IIIEXVYXK
28.0668	10	SIPHAAXHK
28.0670	10	IVXPDXSQK
28.0671	10	LIRXLRXQK
28.0672	10	XTYSPALNK
28.0675	10	TVXAGGXAR
28.0676	10	HISXLTGGR
28.0677	10	XVNXSQFLR
28.0678	10	LIFXHSKKK
28.0679	10	FVLGGXRHK
28.0713	10	TSAIXSVVRR
28.0714	10	HLIFXHSKKK
28.0715	10	LLIRXINXQK
28.0716	10	GIVXPDXSQK
28.0717	10	LLIRXLRXQK
28.0718	10	SLEQRSLHXX
28.0720	10	RIVGGWEXEK
28.0721	10	DIIIEXVYXK
28.0722	10	XVYXKQQLLR
28.0723	10	RAVXGGVLVH
28.0725	10	LTAAHXIRNK
28.0728	10	KAAKWWAGIK
28.0730	10	VVRRXPHHER

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PEPTIDE	AA	SEQUENCE
28.0731	10	LLGIWGXS G K
28.0732	10	TTLFXASDAK
28.0734	10	RTVXAGGXAR
28.0736	10	GTQRXEKXSK
28.0737	10	LVQNANPD K
28.0738	10	VTXNGN I QVR
28.0739	10	DXATMXRHYK
28.0740	10	GLAXHQLXAR
28.0741	10	ALLAXAGLAY
28.0742	10	LLAXAGLAYK
28.0743	10	XVARXPSGVK
28.0745	10	LVEIXTEMEK
28.0746	10	LLNWXM Q IAK
28.0824	11	HMLWKAGI L YK
28.0825	11	HVLWKAGI L YK
28.0826	11	SMLPETTVVRR
28.0827	11	SVLPETTVVRR
28.0828	11	GMDNSVVLSRK
28.0829	11	GVDNSVVLSRK
28.0830	11	GTFNSVVLSRK
28.0369	9	GLAXHQLXA
1259.02	9	DTVDTVLEK
1259.10	9	PVTIGEC P K
1259.14	10	FTAVGKE F NK
1259.16	11	RTLDFHDSNVK
1259.21	11	KTRPILSPLTK
1259.26	11	GTHPSSSAGLK
1259.28	11	ILWILDRLFFK
1259.29	9	WILDRLFFK
1259.30	11	CIYRRFKYGLK
1259.31	9	KSMREEYRK
1259.33	9	YIQMCTELK
1259.37	10	MVMELVRMIK
1259.38	9	VMELVRMIK
1259.41	11	LIRPNENPAHK
26.0023	8	VSFGVWIR
26.0024	8	VSIPWTHK

PEPTIDE	AA	SEQUENCE
26.0026	8	ASF CGSPY
26.0035	9	TSPY ELSLY
26.0036	9	TSIPFLHEY
26.0041	9	FNDPGPGTY
26.0045	9	YVDL GALRY
26.0051	9	DADRSFIEY
26.0055	9	NMDKAVKLY
26.0056	9	TTDNFYRNY
26.0058	9	HSAEALQKY
26.0059	9	LTAGLDFAY
26.0061	9	LTYKYNQFY
26.0062	9	CSNDKSLVY
26.0063	9	RSARASSRY
26.0065	9	ASADKPYSY
26.0067	9	STTAGPNEY
26.0069	9	LSGNGHFPHY
26.0073	9	NTFVQANLY
26.0074	9	GTATYLPPY
26.0081	9	RLDAFRQTY
26.0082	9	KAEVHTFYY
26.0083	9	VAEGDTVIV
26.0084	9	LTEIDIRDY
26.0085	9	HTEFEGQVY
26.0086	9	VSDGGPNLY
26.0092	9	IIEDQYNRY
26.0093	9	FLDQWWTEY
26.0095	9	FVEDPNGKY
26.0096	9	ISDESYRVY
26.0156	9	YLAEADLSY
26.0197	9	ALLAVGATK
26.0198	9	ALNFPGSQK
26.0199	9	AVGATKVPR
26.0203	9	FSVSVSQLR
26.0204	9	GTATLRLVK
26.0205	9	GVS RQLRTK
26.0207	9	LJYRRRLMK
26.0211	9	OLVLHQILK

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PEPTIDE	AA	SEQUENCE
26.0212	9	SSHWRLP R
26.0214	9	TMEVTVYHR
26.0216	9	VLASLIYRR
26.0217	9	VSCQGGLPK
26.0218	9	VVLASLIYR
26.0227	9	GTQCALTRR
26.0251	9	FTIPYWDWR
26.0252	9	GTPEGPLRR
26.0253	9	KSYLEQASR
26.0255	9	LVSLLCRHK
26.0256	9	MVPPFIPLYR
26.0258	9	QTSAGHFPR
26.0259	9	SIFEQWLRR
26.0260	9	SLLCRHKRK
26.0261	9	SSWQIVCSR
26.0267	10	NMQIGGVLY
26.0273	10	RMAQNFAMRY
26.0274	10	FTVQGSLSGY
26.0275	10	QTSPYELSLY
26.0276	10	SSNAILSLSY
26.0280	10	TSQPWWPADY
26.0284	10	VSDVSIIMPY
26.0285	10	ASDAQSANKY
26.0286	10	FTETNLAGEY
26.0287	10	YVDGFEPNGY
26.0291	10	FNDPGPGTYY
26.0296	10	FLDQWWTEYY
26.0299	10	AAEFATETAY
26.0309	10	NAEVVLNQLY
26.0311	10	FVDGDSLFEY
26.0316	10	PSEDAQVAVY
26.0317	10	MSDNIRTGLY
26.0318	10	ESELREILNY
26.0319	10	CMESVRNGTY
26.0320	10	KTENGITRLY
26.0321	10	LTEIDIRDYY
26.0397	10	LLVLMAVVLA

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PEPTIDE	AA	SEQUENCE
26.0424	10	AVVLASLIYR
26.0425	10	GALLAVGATK
26.0426	10	GTATLRLVKR
26.0427	10	HTMEVTVYHHR
26.0428	10	IALNFPGSQK
26.0432	10	QLRALDGGNK
26.0433	10	QVPLDCVLYR
26.0434	10	SLIYRRRLMK
26.0435	10	SSSHWRLPRLPR
26.0438	10	TVSCQGGGLPK
26.0442	10	VVVLASLIYRR
26.0466	10	YVKVLHHTLK
26.0473	10	LIGCWYCRRR
26.0474	10	LLIGCWYCRR
26.0485	10	SSMHNALHIY
26.0504	10	CVSSKNLMEK
26.0510	10	FSSWQIVCSR
26.0511	10	GLVSLLCRHK
26.0518	10	YMVPFIPLYR
26.0535	11	GVWIRTPPAYR
26.0539	11	RLVVDFSQFSR
26.0545	11	TLPETTVVRRR
26.0549	11	LLPIFFCLWVY
	11	STLPETTVVRR
26.0550	11	RAFPHCLAFSY

Table 9

Sequence	AA	Strain	Pos.	Motif	A1	A2.1	A3.2	A11	A24
ALERQDEAL	9	1	15	2.1		<0.0003			
ILLESLPRAV	9	1	93	2.1		0.0004			
VITTKVADL	9	1	101	2.1		<0.0003			
CLGLSYDGL	9	1/3	174	2.1		0.0004			
QIMPKTCFL	9	1	187	2.1		0.0007			
SINCKPEAL	10	1	7	2.1		0.0002			
PLVLTGLEV	10	1	37	2.1		0.0008			
CLLESLPRAV	10	1	92	2.1		0.0003			
AVITTKVADL	10	1	100	2.1		0			
VITTKVADLV	10	1	101	2.1		0			
LILKYPAREPV	10	1/3	114	2.1		0			
EIPGQASESL	10	1	142	2.1		0			
CLGLSYDGLL	10	1/3	174	2.1		0			
AISRKVEL	9	2	101	2.1		0.0003			
RAVELVHFL	9	2	105	2.1		0.16			
RAVELVHFL	9	2	106	2.1		0.0011			
DIQQSLRVL	9	2	143	2.1		0			
SILRVTLAQL	9	2	147	2.1		0.0001			
ALSRKVAEL	9	3	101	2.1		0.0050			
HLYIFATCL	9	3	167	2.1		0.0003			
YIFATCLGL	9	3	169	2.1		0.018			
QIMPKAGLL	9	3	187	2.1		0			

Sequence	AA	Range	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
AISRKVVELV	10	2		101	2.1				0	
MVELVNHFLL	10	2		106	2.1				0.0017	
KIPGALLSRDL	10	2		135	2.1				0	
LISRDILQQSL	10	2		139	2.1				0.0007	
SILPTTANVPL	10	3		63	2.1				0.0035	
DIESEBFQRAL	10	3		93	2.1				0.0001	
AISRKVAVLV	10	3		101	2.1				0.0001	
KVARELWFLL	10	3		105	2.1				0.012	
VISPAASSL	10	3		142	2.1				0	
SIGLVTGIEL	10	3		150	2.1				0.0049	
LAEVVDPIGHL	10	3		159	2.1				0.0005	
FLIIVLVMI	9	1		194	2.1				0.0005	
GLIGDQIM	9	1		181	2.1				0.0051	
SLHCKPPEA	9	1		7	2.1				0.013	<0.0002
AGLGLVQVA	9	1		22	2.1				0.015	<0.0002
CKPPEALEA	9	1		10	Random				<0.0002	
QGEALGLVVC	9	1		19	Random				<0.0002	
VQATSSSS	9	1		28	Random				<0.0002	
PVNLGTLRE	9	1		37	Random				<0.0002	
VPTAGSTDV	9	1		46	Random				<0.0002	
FQSPQGASA	9	1		55	Random				<0.0002	
FPTTINPTR	9	1		64	Random				<0.0002	

Sequence	AA	Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
QRQPSPGS	9	1		73	Random	<0.0002				
SREEEGPST	9	1		82	Random	<0.0002				
AVITRKVAD	9	1		100	Random	<0.0002				
EMLESVIK	9	1		127	Random	<0.0002			0	
YHHCFFPEIF	9	1		136	Random	<0.0002				
GRASESQL	9	1		145	Random	<0.0002				
VFGIDVKEA	9	1		154	Random	<0.0002	<0.0002	0		
DPTGHSYVL	9	1		163	Random	<0.0002				
VTCLGLSYD	9	1		172	Random	<0.0002				
PTGFLFLIV	9	1		190	Random	<0.0002				
LVMIAMGG	9	1		199	Random	<0.0002				
HAPBEEINE	9	1		208	Random	<0.0002				
ELSVNNEVD	9	1		217	Random	<0.0002				
GREHSAYGE	9	1		226	Random	<0.0002				
PRKLLTQDL	9	1		235	Random	0.0002				
VQBKYLEYG	9	1		244	Random	<0.0002				
RCRTVIPHA	9	1		253	Random	<0.0002				
MSSCGVQGP	9	1		262	Random	<0.0002				
ILLESLPRAVI	10	1		93	2.1	0.0002				
FLITIVLIMIA	10	1		194	2.1	0.0003	0.0093	0.0030		
LVFGIDVKEA	10	1		153	2.1	0.0002	<0.0002	0		
EVYDGRHNSA	10	1		222	2.1	0	<0.0002	0		

Sequence	AA	Residue	No.	Pos.	Matrix	A1	A2.1	A3.2	A11	A24
GVQGPSLKPA	10	1		266	2.1		0.0001			
QLVFGIDV	8	1		152	2.1		0			
KLITQDLY	8	1		237	2.1		0.0004			
GLLGDNQI	8	1		181	2.1		0			
DLVQGFLL	8	1		108	2.1		0			
GLSYDGLL	8	1		176	2.1		0.0001			
DLVQEKYL	8	1		242	2.1		0			
LLGDNQIM	8	1		182	2.1		0			
FLIIIVLVM	8	1		194	2.1		0			
ALEAQREA	8	1		15	2.1		0			
TLSBVPTA	8	1		42	2.1		0			
IMPKTGFL	8	1		188	2.1		0.0001			
PVTKAEML	8	1		122	2.1		0			
IVLVMIAN	8	1		197	2.1		0.0001			
AVITKKVA	8	1		100	2.1		0			
EIWBBLSV	8	1		213	2.1		0			
LIIVLVM	8	1		195	2.1		0.0001			
IIIVLVMIA	8	1		196	2.1		0.0002			
SLPRAVITKV	11	1		96	2.1		0.0001			
LLIKYRAREPV	11	1		113	2.1		0.0001			
YLFYGRCRCTV	11	1		248	2.1		0.0006			
ALEAQREALG	11	1		15	2.1		0.0001			

Sequence	AA	Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
FLIVLVVMIAM	11	1		194	2.1		0.0041			
VIGTILBEVPTA	11	1		39	2.1		0.0002			
QLVFGIDVKEA	11	1		152	2.1		0.0001			
AVITKKVADLV	11	1		100	2.1		0			
PVTKAEMLESV	11	1		122	2.1		0			
KVADLVGFLLL	11	1		105	2.1		0.020			
GVQGSPSLKPM	11	1		266	2.1		0			
LVGFLLKTYRA	11	1		109	2.1		0.0004			
LVMIAAMEGCHA	11	1		199	2.1		0.0005			
CILRSULFRAVI	11	1		92	2.1		0.0030			
EALERQQEA	9	1		14	2.1		0	<0.0002	0	
EQEQEALQI	9	1		17	2.1		0		<0.0002	
ATSSSSPL	9	1		30	2.1		0		<0.0002	
ATSSSSPLV	9	1		31	2.1		0.0007			
GTRBEVPTA	9	1		41	2.1		0.013	<0.0002	0	
GASAPPATI	9	1		60	2.1		0		<0.0002	
STSCSLESL	9	1		89	2.1		0.0002			
RAVTTKVA	9	1		99	2.1		0	<0.0002	0	
ITTKVADLV	9	1		102	2.1		0			
RARBPTKA	9	1		118	2.1		0			
KAEMLESVI	9	1		125	2.1		0		<0.0002	
KASERSLQLV	9	1		146	2.1		0.0009			

100

Sequence	AA	Wage Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
PTGHSYVLV	9	1		164	2.1		0			
KTGFLLIVL	9	1		191	2.1		0.0006			
LIVLVNIA	9	1		195	2.1		0	0.0022	0.0006	
LIVLVNIA	9	1		196	2.1		0.0007			
MIAMERGQHA	9	1		201	2.1		0.0005	<0.0002	0.0002	
ETWBELSVW	9	1		213	2.1		0			<0.0002
SAYGEPRKL	9	1		230	2.1		0.0002			
YLEYGRCRT	9	1		248	2.1		0			
EGLGILVCVQA	10	1		21	2.1		0.0005	<0.0002	0	
QATSSSSSPG	10	1		29	2.1		0			<0.0002
VTVAREMELSV	10	1		123	2.1		0			
EGDPGHSIV	10	1		161	2.1		0			
VIGTGLEEYPT	10	1		39	2.1		0.0004			
SAFPITINFT	10	1		62	2.1		0			
GIDVKREADPT	10	1		156	2.1		0			
PTGHSYVLV	10	1	new	164	2.1		0			
FLMOPRALA	9	1	new	265	2.1		0.042	0.0017	0	
LAETSYVKV	9	1	new	272	2.1		0			
YVKYLEIVI	9	1	new	277	2.1		0.0002			
RYREFPPSL	9	1	new	290	2.1		0.0001			
LAETSYVKVL	10	1	new	272	2.1		0			<0.0002
VLEYVIKUSA	10	1	new	260	2.1		0.0002	0.0002	0	

Sequence	AA	Strain	Mag	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
AALREEBEGV	10	1	new		301	2.1			0		
SPHICKPPEEV	9	1	new (a)		7	2.1			0.018		
ANGLYVCYQV	9	1	new (a)		22	2.1			0.012		
LMQGTLSEV	9	1	new (a)		38	2.1			0.13		
LQLVFGIDV	9	1	new		151	2.1			0.0004		
GLSYDGILG	9	1	new		176	2.1			0		
GLSYDGILV	9	1	new (a)		176	2.1			0.0047		
LIGDNQIIMP	9	1	new		182	2.1			0.0001		
LIGDNQIIMV	9	1	new (a)		182	2.1			0.043		
WEELSVMEV	9	1	new		215	2.1			0		
WEELSVMEV	9	1	new (a)		215	2.1			0.041		
RKLLTQDLV	9	1	new		236	2.1			0		
YBFLNGPRA	9	1	new		262	2.1			0		
YMFLNGPRV	9	1	new (a)		262	2.1			0.22		
ATSSSSSPLY	10	1	new		30	2.1			0		
ATSSSSSPYL	10	1	new		31	2.1			0		
KMADLUGFLV	10	1	new (a)		105	2.1			1.5		
VADLUGFLL	10	1	new		106	2.1			0.0008		
SESLQLVFGI	10	1	new		148	2.1			0		
WMTTCGLSV	10	1	new (a)		170	2.1			0.30		
QIMPRTGFLI	10	1	new		187	2.1			0.0009		
QMMPKTGFLV	10	1	new (a)		187	2.1			0.050		

Sequence	AA	Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
KTGRFLIIVV	10	1	new	191	2.1		0.0012			
LIVIVYMIAM	10	1	new	195	2.1		0.0003			
VNLAMEGGHV	10	1	new (a)	200	2.1		0.053			
SPAGEPRKIL	10	1	new	230	2.1		0		0.0008	
ALAFETSYVKVL	11	1 N		270	2.1		0.012			
KMVELVHFLL	11	2		52	2.1		0.67			
ELMEBVDPIGH	11	3		105	2.1		0.026			
HLYIFATCLGL	11	3		114	2.1		0.041			
LLIKYRAREPPV	11	3		60	2.1		0.0001			
QLVFGIELMEV	11	3		99	2.1		0.34			
IMPKGAGLIIIV	11	3		135	2.1		0.013			
VLNTCLGLSYDGL	13	1 n	E6	170	2.1		0.0017			
KLIJTDQDLYQEKYL	13	1 n	E6	237	2.1		0.0060			
DIVQEKYLEYRQV	13	1 n	E6	242	2.1		0			
SLFRAVITKKVADLV	15	1 n	POL	96	2.1		0.0004			
DLESEFQRAISRKMV	15	2	POL	40	2.1		0			
MLGSSVVGNNQXFPPV	15	3	POL	75	2.1		0.012			
GASSFSTTI	9	2		60	2.1		0		0.0002	
DLESEFQRA	9	2,3		93	2.1		0			
QAAISRKMV	9	2		99	2.1		0			
KAEMLASSVL	9	2		125	2.1		0		0	
KASBYLQLW	9	2		146	2.1		0.011			

Sequence	AA	Strain	Mag.	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
QIVFGIEVV	9	2			152	2.1			0.0038		
VVPISHLHY	9	2			162	2.1			0.0002		
PISHLYILV	9	2			164	2.1			0.0005		
HIXLYLYCL	9	2			167	2.1			0.0034		
YIINTCLAL	9	2			169	2.1			0.0014		
GLIADNQYM	9	2			181	2.1			0.0038		
QYDPKTQIL	9	2			187	2.1		0			
VMPKTKLII	9	2			188	2.1			0.0010		0.230
KTGLLILVL	9	2			191	2.1			0.0002		
GLLTKVIAI	9	2,3			193	2.1			0.0002		
LLIVLIAII	9	2,3			194	2.1			0.0001		
LLIVLIAIA	9	2,3			195	2.1			0.0008		
IIVLIAIAI	9	2			196	2.1			0.0009		
IIAIKGDCA	9	2			201	2.1		0			
GASSLPTTM	9	3			60	2.1		0		0.0010	
QALSRKVA	9	3			99	2.1		0			
VAEVLVHFL	9	3			106	2.1		0		0.039	
KAEMLGSTW	9	3			125	2.1		0			
KASSSIQLV	9	3			146	2.1			0.0005		
QIVFGIELM	9	3			152	2.1			0.0010		
PIGHLYIFR	9	3			164	2.1		0			
IMPKAGLAI	9	3			188	2.1			0.0064		

Sequence	AA	Strain	MoL	Pos.	Motif	A1	A2.1	A3.2	A11	A24
KAGLLIVL	9	3		191	2.1		0.0002		0	
LLIARIGDCA	9	3		201	2.1		0		0	
EALEAQEAL	10	1	new	14	2.1		0		0	
EAQDEAQGLV	10	1	new	17	2.1		0		0	
DLESHFQAAI	10	2		93	2.1		0		0	
AAISRKVTEL	10	2		100	2.1		0		0	
VIPSKASEYL	10	2		142	2.1		0.0014			
YIQLVFGIEV	10	2		150	2.1		0.37			
LYFGIEVVEV	10	2		153	2.1		0.012			
GIEVVVEVPI	10	2		156	2.1		<0.0002			
VVBBVPISHL	10	2		159	2.1		<0.0002			
EVVPISHLYI	10	2		161	2.1		<0.0002			
VVPISHLYIL	10	2		162	2.1		0.0002			
PISHLYILV	10	2		164	2.1		0.0003			
QVAPKTLILLI	10	2		187	2.1		0.0002			
VMPKTLILLI	10	2		188	2.1		0.0009		0.058	
KTGLLIVLVA	10	2		191	2.1		<0.0002			
GLLIVLVAII	10	2,3		193	2.1		0.0005			
LLIVLVAIIA	10	2,3		194	2.1		<0.0002			
LLIVLVAIIAI	10	2		195	2.1		0.0013			
AIIAIGDCA	10	2		200	2.1		0.0023			
AAISRKVTEL	10	3		100	2.1		0.0007		0	

Sequence	AA	Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
VAELVTHFLL	10	3		106	2.1		0.0009			0.00018
VTKAEMIGSV	10	3		123	2.1		<0.0002			
GIEELMEVDPI	10	3		156	2.1		<0.0002			
EVDPIGHLYI	10	3		161	2.1		<0.0002			
PIGHLYIFAT	10	3		164	2.1		0.0003			
QIMPKGALLI	10	3		187	2.1		0.0006			
IMPKGALLI	10	3		188	2.1		0.0015			
KAGLLIIVLA	10	3		191	2.1		<0.0002			
AIARBGDCA	10	3		200	2.1		<0.0002			
FLNGPRLI	9	2		271	A02					
GLEARGEAL	9	3		15	A02					
ERGEALGL	9	3		17	A02					
ALGLVNGQRA	9	3		22	A02/A03					
GLVGAQAPA	9	3		24	A02/A03					
LVGAQAPAT	9	3		25	A02					
PATEQERA	9	3		31	A02/A03					
ERASSSSSTL	9	3		37	A02					
AASSSSSTLV	9	3		38	A02					
LVETVLGEV	9	3		45	A02					
EVTLGEVPA	9	3		47	A02/A03					
VTLGEGVPA	9	3		48	A02/A03					
NIWEEELSVL	9	3		220	A02					

Sequence	AA	Strain	Nag	Nol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
SIIGDPKKL	9	3			237	A02					
ILGDPKKL	9	3			238	A02					
FLWGPRALV	9	3			271	A02					
RALVETSYV	9	3			276	A02					
LVETSYVTV	9	3			278	A02					
YVKVLLHHMV	9	3			283	A02					
KVLLHHMVVKI	9	3			285	A02					
EARGGRALIVY	10	3			17	A02					
ERLGLANGQQA	10	3			21	A02/A03					
GLVGRQAPAT	10	3			24	A02					
QAPATERQRA	10	3			29	A02/A03					
ERASSSSSTLV	10	3			37	A02					
TLVEVTIGEV	10	3			44	A02					
EVTIGEVPA	10	3			47	A02/A03					
EVFEGREDSI	10	3			229	A02					
SIIGDPKKL	10	3			237	A02					
ILGDPKKL	10	3			238	A02					
ALVETSYVKV	10	3			277	A02					
LVETSYVKVL	10	3			278	A02					
MVKISGGPHI	10	3			290	A02					
LVLGTLSEEV	9	1			38	2.1	<0.0006	0.032	0	0	0.0003
KVADLIVQPL	10	1			105	0.0005	0.041	0.0039	0.0030	0.0070	

Sequence	AA	Page	Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
LVFGIRLMEV	10	3		153	2.1		0.17				
ILLWQPIPV	9	3				<0.0007	1.4	0.0048	0.0048	0	
EVDPIGHLY	9	3				3.7				0.0022	
KMVELVHFL	9	2				<0.0007	0.13	0.0007	0	0.0043	
KVQTELVHFL	10	2		105		<0.0008	0.071	0.0004	0.0001	0.0008	
LVFGIRLMEV	10	3				0.0030	0.065	0.0007	0	0	
KVABLVHFL	9	3		105	2.1	0	0.073	0.011	0.0047	0.0005	
CILLESLIFRA	9	1		92	2.1	0.0001	0.073	0	0.0002	0	
VMIAAMEGGHA	10	1		200	2.1	<0.00008	0.0023	0	0	0	
MLESVIKNYK	10	1				0	0	0.034	0.0045	0	
ETSYVKVLEY	10	1				0.075	0	0.0009	0.0004	0	
KYLEYVKV	9	1	new	279	2.1	<0.0005	0.095	0.022	0.015	0	
PLNGPRALIA	9	1				<0.0006	0.027	0.0015	0	0	
ALPREEEGCV	9	1		302	2.1	<0.0006	0.0056	0	0	0	
ALAETSYVKV	10	1		271		<0.0007	0.017	0.0011	0.0029	0	
YVIKVSYARV	9	1		283	2.1	0.0005	0.018	0	0	0	
RALASTSYV	9	1		270	2.1	<0.0006	0.014	0.0003	0.0005	0	
ALAETSYVK	9	1				<0.0006	0.0002	0.17	0.39	0	
VLGTLSEEV	8	1		39	2.1	<0.0007	0.0088	0	0	0	
SLQLVPGI	8	1		150	2.1	<0.0007	0.0094	0	0.0001	0	
IILLESLIFRA	8	1		93	2.1	<0.0004	0.0017	0.0003	0	0.0001	
PLILKTYRA	8	1		112	2.1	0.0036	0.0007	0.0003	0.0001	0	

Sequence	AA	Mass	Strain	No.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
GLVCVQAA	8	1		24	2.1	0.0016	0.0008	0.0008	0	0	
VLVTCIGL	8	1		170	2.1	<0.0007	0.0010	0.0001	0	0	
KVADLNGFL	9	1		105	2.1	<0.0008	0.0091	0.0013	0.0005	0	
YLVNTCLL	9	1		169	2.1						
IMPKTGFLI	9	1		188	2.1	<0.0008	0.0035	0	0	0	3.2
GLIADNQIM	9	1			A2.1	<0.0008	0.0054	0	0	0.0002	
GLVCVQAA	9	1		24	2.1	0.0030	0.0007	0.0026	0	0.0001	
VADLNGFL	9	1		106	2.1	0.032	0.0011	0.0054	0.0008	0.0007	
YLYYGRCKTV	10	1		248	2.1	0.0008	0.0097	0.0001	0	0	
SLQLVFGIDV	10	1		150	2.1	0.0028	0.0047	0.0013	0.0001	0.0001	
IMPKTGFLII	10	1		188	2.1	<0.0008	0.0007	0	0	0.050	
ALGIVCVQAA	10	1		22	A2.1	0.0011	0.0002	0.0003	0	0	
EIMERLSVMEV	11	1		213	A2.1	0.0007	0.013	0.0001	0.0001	0	
FLIVLVMAM	11	1			A2.1	0.023	0.0031	0.016	0.0014	0.0011	
VIPHAMSSCTV	11	1		257	2.1	<0.0009	1.4	0	0	0	
CILBSCFRAVI	11	1			A2.1	0.079	0.0017	0.058	0.0005	0.0008	
QIMPKTGFLII	11	1		167	2.1	<0.0009	0.0003	0	0	0.0030	
GFLAJKTYA	9	1					0.0004	0.0002			
CFPEKFGKA	9	1						0	0		
FFFFPSLREA	9	1						0	0		
FFFFPSLREA	9	1						0	0		
RSLHCKPBEA	10	1						0.0001	0.0008		

Sequence	AA	Mass	Strain	Mol.	Pos.	Motif	A1	A2.1	A3.2	A11	A24
EFLMGPRALA	10	1							0	0	
RFFFPSLREA	10	1							0.0004	0	
FFPPSLREAA	10	1							0	0	

Sequence	Antigen	Strain	Molecule	Position	Motif	A1	A2	A3	A11	A24	Max.
					Binding						
ALFLGFLGAA	HIV	MN	gp160	518	A02	0.4950					0.4950
MLQLTVNGI	HIV	MN	gp160	566	A02	0.2450					0.2450
RVTEVLQRA	HIV	MN	gp160	829	A02	0.1963					0.1963
KLTPLCVTL	HIV	MN	gp160	120	A02	0.1600					0.1600
LLIAARIVEL	HIV	MN	gp160	776	A02	0.1550					0.1550
SLLNATDIAV	HIV	MN	gp160	814	A02	0.1050					0.1050
ALFLGFLGAA	HIV	MN	gp160	518	A02	0.0945					0.0945
HMLQLTVNGI	HIV	MN	gp160	565	A02	0.0677					0.0677
LLNATDIAV	HIV	MN	gp160	815	A02	0.0607					0.0607
ALLYKLDIV	HIV	MN	gp160	179	A02	0.0362					0.0362
WLWYKIKIFI	HIV	MN	gp160	679	A02	0.0355					0.0355
TIVHLNESV	HIV	MN	gp160	288	A02	0.0350					0.0350
LLQYWSQL	HIV	MN	gp160	810	A02	0.0265					0.0265
IMIVGGVLGL	HIV	MN	gp160	687	A02	0.0252					0.0252
LLYKLDIVSI	HIV	MN	gp160	180	A02	0.0245					0.0245
FLAIIWDL	HIV	MN	gp160	753	A02	0.0233					0.0233
TLQCKIKQII	HIV	MN	gp160	415	A02	0.0200					0.0200
GLVGLRIVFA	HIV	MN	gp160	692	A02	0.0195					0.0195
FLGAAGSTM	HIV	MN	gp160	523	A02	0.0190					0.0190
LLSLWDQSL	HIV	MN	gp160	107	A02	0.0179					0.0179
TWNGIKQQLQA	HIV	MN	gp160	570	A02	0.0150					0.0150
LLGRRGWEV	HIV	MN	gp160	785	A02	0.0142					0.0142
AVLSTIVNVR	HIV	MN	gp160	701	A02	0.0132					0.0132

Sequence	Antigen	Strain	Molecule	Position	Motif	A1	A2	A3	A11	A24	Max.
						Binding	Binding	Binding	Binding	Binding	Binding
FIMIVGGGV	HIV	MN	gp160	686	A02	0.0131	—	—	—	—	0.0131
LLNATDIAVA	HIV	MN	gp160	815	A02	0.0117	—	—	—	—	0.0117
FLYGALLLA	PLP	Human		80	A02	1.9000	—	—	—	—	1.9000
SLLTTFMIAA	PLP	Human		253	A02	0.5300	—	—	—	—	0.5300
FMIAATYNFAV	PLP	Human		257	A02	0.4950	—	—	—	—	0.4950
FRMYGVLPWI	PLP	Human		205	A02	0.1650	—	—	—	—	0.1650
IAATYNFAV	PLP	Human		259	A02	0.0540	—	—	—	—	0.0540
GLLECCARCLV	PLP	Human		2	A02	0.0515	—	—	—	—	0.0515
YALTIVWLL	PLP	Human		157	A02	0.0415	—	—	—	—	0.0415
ALTIVWLLV	PLP	Human		158	A02	0.0390	—	—	—	—	0.0390
FLYGALLL	PLP	Human		80	A02	0.0345	—	—	—	—	0.0345
SLCADARMYGV	PLP	Human		199	A02	0.0140	—	—	—	—	0.0140
LLVFACSAV	PLP	Human		164	A02	0.0107	—	—	—	—	0.0107

Table 10

AA	SEQUENCE	SOURCE
9	YIFATCLGL	MAGE 3 169
9	IMPKTGFLI	MAGE 1 188
10	IMPKTGFLII	MAGE 1 188
15	MLGSVVGNGWQYFFPV	MAGE 3 POL 75
9	VMPKTGLLI	MAGE 2 188
9	IMPKAGLLI	MAGE 3 188
10	IMPKAGLLII	MAGE 3 188
9	RLWHYPCTV	HCV Env2 614
9	RLWHYPCTI	HCV Env2 614
9	FLLLADARI	HCV Env2
9	GVWPLLLLL	HCV Env2 792
15	GMWPLLLLL	HCV Env2 792
9	YLNTPGLPV	HCV NS3/NS4 1542
9	YMNTPGLPV	HCV NS3/NS4 1542
9	VILDSFDPL	HCV NSS 2251
9	ILMTHFFSI	HCV NSS 2843
20	ILMTHFFSV	HCV NSS 2843
9	LMAVVVLASL	gp100 606
9	SLSLGFLFL	PAP 13
10	YMIMVKCWMI	c-ErbB2 952
10	GLHGQDLFGI	PAP 196
25	AILSVSSFL	P. falciparum CSP 6
9	GLIMVLSFL	P. falciparum CSP 425
9	VLLGGVGLV	P. falciparum EXP-1 91
9	GLLGNVSTV	P. falciparum EXP-1 83
9	LLGNVSTVL	P. falciparum EXP-1 84
30	VLAGLLGNV	P. falciparum EXP-1 80

AA	SEQUENCE	SOURCE
9	KILSVFFLA	<i>P. falciparum</i> EXP-1 2
9	FLIFFDLFL	<i>P. falciparum</i> TRAP 14
9	LJFFDLFLV	<i>P. falciparum</i> TRAP 15
9	FMKAVCVEV	<i>P. falciparum</i> TRAP 230
5	LLMDCSGSI	<i>P. falciparum</i> TRAP 51
10	ILSVSSFLFV	<i>P. falciparum</i> CSP 7
10	VLLGGVGLVL	<i>P. falciparum</i> EXP-1 91
10	GLLGNVSTVL	<i>P. falciparum</i> EXP-1 83
10	FLIFFDLFLV	<i>P. falciparum</i> TRAP 14
10	GLALLACAGL	<i>P. falciparum</i> TRAP 507
10	KIWEELSML	MAGE2 220
15	TLMMSAMTNL	Prost.Ca PAP 112
15	LLLARAASL	Prost.Ca PAP 6
15	ALDVYNGLL	Prost.Ca PAP 299
15	VTFWIGAAPL	PSA 8
10	ALIETSYVKV	MAGE2 277
10	SLSLGFLFL	Prost.Ca PAP 13
10	RTLMSAMTNL	PAP 111
20	FLPSDFFPSV(CONH2)	HBc 18-27
20	FLPSDFFPSV-NH2	HBc 18-27
20	ILGFVFTLT-NH2	Flu Matrix 59-67
20	KGILGFVFTL-NH2	Flu Matrix 57-66
25	FLPSDFFPSVR	HBc 18-28
25	FLPSDFFPS	HBc 18-26
25	GILGKVFTL	Flu Matrix 58-66 analog
25	FLSKQYLN	HBV polymerase
25	KLQCVPLHV	PSA 166-174 P/D

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AA	SEQUENCE	SOURCE
9	KLQCVPLHV	PSA 166-174 P/D
9	KLQCVPLHV	PSA 166-174 P/D
9	KLYEIVAKV	A2.1 consensus
9	KLAEYVAKV	A2.1 consensus
9	KLAEIVYKV	A2.1 consensus
9	TLTSCNTSV	HIV gp 120 env. RE trans. 197
9	ALMEKIYQV	A2.1 consensus peptide
9	ALSEKIYQV	A2.1 consensus peptide
9	FLMSYFPSV	941.01 9-mer analog
9	FLPSYFPSV	941.01 9-mer analog
10	FLMSDYFPSV	941.01 M2 analog
9	FLCYFALV	Chiron consensus
9	FMYCYFALV	Chiron consensus
10	SLVGFPGILCV	Chiron consensus
10	SLMGCGLFVV	Chiron consensus
8	GLLGPLLV	HBVadr-ENV
9	AMAKAAAAI	A2.1 poly-A
10	MMWYWGPSLY	HBV
9	FLPSYFPSA	analog of 994.02: chiron comb
9	FAPSYFPSV	analog of 994.02: chiron comb
9	FLPSYFPSS	analog of 994.02: chiron comb
9	FSPSYFPSV	analog of 994.02: chiron comb
9	IMPKTGFLL	MAGE-1
9	VADLVGFLL	MAGE-1
11	EIWEELSVMEV	MAGE-1
11	FLIIVLVMIAM	MAGE-1
11	VIPHAMSSCGV	MAGE-1
11	CILESCFRAVI	MAGE-1
9	YIFATCLGL	MAGE3

AA	SEQUENCE	SOURCE
9	YIFATCLGL	MAGE3
11	KMVELVVHFLLL	MAGE2 112-122
11	HLFIYATCLGL	MAGE3 174-184
9	GLQDCTMLV	HCV NS5 2727-2735
8	TLGIVSPI	HPV, analog of 1088.01
8	TLGIVXPI	HPV, analog of 1088.01
10	FLLAQFTSAI	HBV POL 513
11	VLLDYQGMLPV	HBV env
11	CILLCLIFLL	HBV env
10	FLGGSPVCL	HBV env
11	TVIEYLVSFGV	HBV core 114-124
11	TVLEYLVSFGV	HBV core 114-124
10	FLLAQFTSAI	HBV pol
15	GLYSSTVPI	HBV pol
9	GLYSSTAPI	HBV pol
9	GLDVLTAKV	HIV form VIN.
9	RILGAVAKV	HIV form VIN.
9	LLFGYPVYV	HTLV, tax 11-19
9	ALFGYPVYV	tax 11-19, SAAS
20	LLFGAPVYV	tax 11-19, SAAS
9	LLFGYAVYV	tax 11-19, SAAS
9	LLFGYPVAV	tax 11-19, SAAS
9	AAGIGILTV	MART1 27-35
9	GILTVILGV	MART1 31-39
25	ILTVILGV1	MART1 32-40
9	VILGVILLI	MART1 35-43
9	ALMDKSLHV	MART1 56-64
10	TVILGVILLI	MART1
10	LLDGATATRL	MART1
30	ILSVSSFLFV	Plas. falcip. CSA-A 7-16
9	GLIMVLSFL	Plas. falcip. CSA-A 401-409

AA	SEQUENCE	SOURCE
9	IMVLSFLFL	Plas. falcip. CSA-A 403-411
10	FLIFFDLFLV	Plas. falcip. TRAP-A 14-23
9	FMKAVCVELV	Plas. falcip. TRAP-A 200-207
9	IMPGQEAGL	gp100
9	GLGQVPLIV	gp100
9	LMAVVLASL	gp100
9	RLMKQDFSV	gp100
9	HLAVIGALL	gp100
9	LLAVGATKV	gp100
10	MLGTHTMEV	gp100
10	LLDGTATLRL	gp100
10	VLYRYGSFSV	gp100
10	VLPSPACQLV	gp100
10	SLADTNSLAV	gp100
15	VLMAVVLASL	gp100
10	LMAVVLASLI	gp100
10	RLDCWRGGQV	gp100
10	AMLGTHTMEV	gp100
10	ALDGGNKHFL	gp100
20	YLEPGPVTA	gp100
10	LLNATAIAVA	
11	SLLNATAIAVA	
9	KTWGQYWQV	gp100
9	ITDQVPPFSV	gp100
25	YLEPGPVTA	gp100
10	LLDGTATLRL	gp100
10	VLYRYGSFSV	gp100
10	ALDGGNKHFL	gp100
9	GILTVILGV	MART1 31-39
30	YMNGTMSQV	Human Tyrosinase
9	MLLAVLYBL	Human Tyrosinase
9	LLWSFQTSA	Human Tyrosinase

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AA	SEQUENCE	SOURCE
9	YLTAKHTI	Human Tyrosinase
9	FLPWHRLFL	Human Tyrosinase
9	FLLRWEQEI	Human Tyrosinase
9	RIWSWLLGA	Human Tyrosinase
9	LLGAAMVGA	Human Tyrosinase
9	AMVGAVLTA	Human Tyrosinase
9	VLTALLAGL	Human Tyrosinase
9	ALLAGLVSL	Human Tyrosinase
9	LLAGLVSL	Human Tyrosinase
10	BLLWSFQTSA	Human Tyrosinase
10	WMHYYVSMDA	Human Tyrosinase
10	FLPWHRLFLL	Human Tyrosinase
10	WLLGAAMVGA	Human Tyrosinase
10	AMVGAVLTA	Human Tyrosinase
10	VLTALLAGLV	Human Tyrosinase
10	TALLAGLVSL	Human Tyrosinase
10	ALLAGLVSL	Human Tyrosinase
9	NLTDALLQV	P. falciparum SSP2 132
9	SAWENVKNV	P. falciparum SSP2 218
10	FLIFFDLFLV	P. falciparum SSP2 14
9	NLNDNAIHL	P. falciparum SSP2 80
10	YLLMDCSGSI	P. falciparum SSP2 51
9	TLQDVSVLEV	controls

Table 11

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AA	SEQUENCE	SOURCE
9	ALYWFRGI	HPV 6b/11 E1 319
	LLDGNPMSI	HPV 6b/11 E1 540
9	NAWGMVLLV	HPV 6b/11 E1 270
9	SLYAHIQWL	HPV 6b/11 E1 260
9	TLIKCPPLL	HPV 6b/11 E1 556
9	GIYDALFDI	PSMAg 707
9	YLSGANLNLL	CEA 605
9	VLYGPDPTI	CEA 589
9	IMIGVLVGV	CEA 691
9	LLTFWNPPT	CEA 24
9	KLTEMVQWA	HPV 6b/11 E1 357
9	YMDTYMRNL	HPV 6b/11 E1 532
10	NLLDGNPMSI	HPV 6b/11 E1 539
10	SLYAHIQWLT	HPV 6b/11 E1 260
10	TLIKCPPPLV	HPV 6b/11 E1 556
10	MVFELANSIV	PSMAg 583
10	YLWWVNNQSL	CEA 176
10	YLWWVNNQSL	CEA 354
10	YLWWVNGQSL	CEA 532
10	GIMIGVLVGV	CEA 690
10	VLYGPDAPTI	CEA 233
10	KLIEPLSLYA	HPV 6b/11 E1 254
10	WLCAGALVLA	PSMAg 20
10	IMIGVLVGVVA	CEA 691

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AA	SEQUENCE	SOURCE
9	YLYQLSPPI	HTLV-I tax 155
9	LLFEEYTNI	HTLV-I tax 307
9	QLGAFLTNV	HTLV-I tax 178
9	TLTAWQNGL	HTLV-I tax 226
9	ALQFLIPRL	HTLV-I tax 67
9	TLGQHLPTL	HTLV-I tax 123
9	FAFKDLFVV	HPV 18 E6 47
9	RLLQLLFRA	GCDFP-15 2
9	CMVVKTYLI	GCDFP-15 65
9	LLLVLCLQL	GCDFP-15 15
9	ILYAHIQCL	HPV18 E1 266
9	SLACSWGMV	HPV16 E1 266
9	CLYLHQSL	HPV16 E1 259
9	YLVSPLSDI	HPV16 E1 90
9	VMFLRYQGV	HPV16 E1 443
9	KLLSKLLCV	HPV16 E1 292
9	ALDGPNISI	HPV18 E1 546
9	AVFKDTYGL	HPV18 E1 216
9	LLTTNIHPA	HPV18 E1 570
9	LLQQYCLYL	HPV16 E1 254

AA	SEQUENCE	SOURCE
9	AMLAKFKEL	HPV16 E1 206
9	ALDGNLVSM	HPV16 E1 539
9	FLGALKSFL	HPV18 E1 463
9	FIHFIQGAV	HPV18 E1 497
10	TLLLVLICLQL	GCDFP-15 14
10	LLFRASPATL	GCDFP-15 6
10	SLMKFLQGSV	HPV16 E1 489
10	SLACSWGMVV	HPV16 E1 266
10	FLQGSVICFV	HPV16 E1 493
10	FIQGAVISFV	HPV18 E1 500
10	KLLCVSPMCM	HPV16 E1 296
10	FILYAHIQCL	HPV18 E1 265
10	FVNSTSHFWL	HPV18 E1 508
10	ILLTTNIHPA	HPV18 E1 569
15	TLLQQYCLYL	HPV16 E1 253
9	GLLGWSPQA	HBV ENV 62
9	GLACHQLCA	HER2/neu
9	ILDEAYVMA	HER2/neu
9	SIISAVVGI	HER2/neu
9	VVLGVVFGI	HER2/neu
9	YMIMVKCWM	HER2/neu
10	ALCRWGLLA	HER2/neu
10	QLFEDNYALA	HER2/neu

AA	SEQUENCE	SOURCE
9	HMWNFISGI	HCV consensus
9	VIYQYMDDL	HIV POL 358.
9	SLYNTVATL	HIV GAG 77
10	TVWGIKQLQA	HIV ENV 735
9	LILLEAGALV	MSH 99
9	VLETAVGLL	MSH 92
9	CLALSDLLV	MSH 79
9	FLSLGLVSL	MSH 45
9	SLVENALVV	MSH 52
9	AIIDPLIYA	MSH 291
9	FLCWGPFFL	MSH 251
9	FLALIICNA	MSH 283
9	TILLGIFFL	MSH 244
9	RLLGSLNST	MSH 9
9	SLYNTVATL	HIV p17/5B 77-8
9	VIYQYMDDL	HIV RT/50A 346-
9	ILKEPVHGV	HIV RT/IV9 476-

Table 12

PEPTIDE NO.	PEPTIDE LENGTH	SEQUENCE
1237.01	9	FLWGPQALV
1237.02	9	FLWGPNALV
1237.03	9	FLWGPHALV
1237.04	9	FLWGPKALV
1237.05	9	FLWGPFLAV
26.0158	9	AVIGALLAV
26.0172	9	LLHLAVIGA
26.0186	9	SLADTNSLA
26.0192	9	VMGTTLAEM
26.0240	9	LLAVLYCLL
26.0383	10	FLRNQPLTFA
26.0390	10	HLAVIGALLA
26.0395	10	LAVIGALLAV
26.0418	10	TLAEMSTPEA
26.0423	10	YLAEADLSYT
26.0497	10	MLLAVLYCILL
1183.10	10	VLYRYGSFSV
27.0007	9	ILSSLGLPV
27.0012	9	ILFLGVVFL
27.0019	9	GLYGAQYDV
27.0022	9	FVVALIPLV
27.0023	9	GLMTAVYLV
27.0027	9	ALVLLMLPV
27.0028	9	ILLSIARVV
27.0029	9	SLYFGGICV
27.0030	9	QLIPCMDVV
27.0031	9	VLQQSTYQL
27.0032	9	AIHNVVHAI
27.0034	9	GLHGVGVSV
27.0035	9	GLVDFVKHI
27.0036	9	LLFRFMRPL
27.0038	9	LMLPGMNGI
27.0043	9	TVLRFVPPL
27.0044	9	MLGNAPSVV
27.0050	9	YLDLALMSV
27.0064	9	RMPEAAPPV

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PEPTIDE NO.	PEPTIDE LENGTH	SEQUENCE
27.0082	9	FLLPDAQSI
27.0083	9	MTYAAPLFV
27.0088	9	LLPLGYPPFV
27.0089	9	GLYYLTTEV
27.0090	9	MALLRLPLV
27.0091	9	RLPLVLPLAV
27.0093	9	RMFAANLGV
27.0095	9	RLLDDDTPEV
27.0096	9	YLYVHSPAL
27.0100	9	GLYLSQIAV
27.0101	9	YLSQIAVLL
27.0102	9	SLAGFVRML
27.0137	10	ATYDKGILTV
27.0146	10	KIFMLVTAVV
27.0151	10	FLLADERVRV
27.0153	10	MLATDLSLRV
27.0154	10	RLQPQVGWEV
27.0161	10	FLMPVEDVFI
27.0165	10	RMSRVTTFTV
27.0168	10	LALVLLMLPV
27.0169	10	ALVLLMLPVV
27.0170	10	GIVSGILLSI
27.0171	10	SLYFGGICVI
27.0173	10	QLIPCMDVVL
27.0181	10	LLFRFMRPLI
27.0183	10	VLLEDGGVEV
27.0184	10	AMPAYNWMTV
27.0186	10	GLAGTVLRFV
27.0188	10	VLIAFGRFPI
27.0189	10	FLTC DANLAV
27.0197	10	AIAWGAWGEV
27.0204	10	LLLETSWEAI
27.0217	10	RMPEAAPPVA
27.0223	10	WMAETTLGRV
27.0226	10	AMALLRLPLV
27.0229	10	FMSLAGFVRM
27.0266	11	SLLTEVETVVL

PEPTIDE NO.	PEPTIDE LENGTH	SEQUENCE
27.0268	11	GILGFVFTLTV
27.0269	11	VLDVGDAYFSV
27.0271	11	KIWEELSMLEV
27.0272	11	STLVEVTLGEV
27.0273	11	GLAPPQHILRV
27.0274	11	HLIRVEGNILRV
27.0005	9	YLLALRYLA
27.0013	9	GLYRQWALA
27.0017	9	LLWQDPVPA
27.0040	9	ALLSDWLPA
27.0045	9	WLLIDTSNA
27.0046	9	MLASTLTDA
27.0081	9	YLSEGDMAA
27.0094	9	LLACAVIHA
27.0144	10	LLCCSGVATA
27.0191	10	LLATVFKLTA
27.0192	10	KLTADGVLTA
27.0195	10	GLGGIQLFFA
28.0064	8	TLGIVXPi
28.0065	8	ALGTTKYA
28.0293	9	FLLTRILTV
28.0294	9	ALMPLYACV
28.0295	9	LLAQFTSAV
28.0296	9	LLPFVQWVFV
28.0297	9	FLLAQFTSV
28.0298	9	KLHLYSHPV
28.0299	9	KLFLYSHPI
28.0300	9	LLSSNLSWV
28.0301	9	FLLSLGIHV
28.0302	9	MMWYWGPSV
28.0303	9	VLQAGFFLV
28.0304	9	FLLPIFFCV
28.0305	9	FLLPIFFCL
28.0306	9	VLLDYQQMV
28.0307	9	YMDDVVVLGV
28.0308	9	YMFDVVLGA
28.0309	9	GLLGWSPOV

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PEPTIDE NO.	PEPTIDE LENGTH	SEQUENCE
28.0342	9	YMIMVKXWM
28.0343	9	YIFATXLGL
28.0345	9	SLHXKPEEA
28.0346	9	ALGLVXVQA
28.0348	9	LLMDXSGSI
28.0349	9	FAFRDLXIV
28.0352	9	GTLGIVXP1
28.0353	9	TLGIVXP1X
28.0354	9	LLWFHISXL
28.0355	9	KLTPPLXVTL
28.0356	9	ALVEIXTEM
28.0357	9	LTFGDXFKL
28.0359	9	KLQXVDLHV
28.0360	9	FMKAVXVEV
28.0361	9	LLQQYXLYL
28.0362	9	XLYLHIQSL
28.0363	9	SLAXSWGMV
28.0364	9	ILYAHIQXL
28.0365	9	KLLSKLLXV
28.0366	9	PLLPIFFXL
28.0367	9	TLIKXPPLL
28.0368	9	ALMPLYAXI
28.0370	9	XILESLFRA
28.0609	10	FLLAQFTSAV
28.0610	10	YLHTLWKAGV
28.0611	10	YLFTLWKAGI
28.0612	10	YLLTLWKAGI
28.0613	10	LLFYQGMLPV
28.0614	10	LLLYQGMLPV
28.0615	10	LLVHQAGFFV
28.0616	10	ILLLCLIFLV
28.0650	10	ALXRWGLLL
28.0651	10	KLPDLXTEL
28.0652	10	HLYQQGXQVV
28.0653	10	XILESLFRA
28.0654	10	KLQXVDLHV
28.0655	10	YIFATXLGL

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PEPTIDE NO.	PEPTIDE LENGTH	SEQUENCE
F111.01	9	SLYNTVATL
F111.02	9	ALYNTVATL
F111.04	9	SLANTVATL
F111.06	9	SLFNAVATL
F111.07	9	SLFNLLATL
F111.10	9	SLFNTIAVL
F111.11	9	SLFNAVAVL
F111.09	9	SLFNTIVVL
F111.12	9	SLFNAIAVL
F111.13	9	SLFNTVAVL
F111.14	9	SLFNTVCVI
F111.15	9	SLHNTVATL
F111.17	9	SLHNTVAVL
F111.18	9	SLYATVATL
F111.19	9	SLYNAVATL
F111.21	9	SLYNTAATL
F111.22	9	SLYNTIAVL
F111.23	9	SLYNTSATL
F111.25	9	SLYNTVAVL
F111.26	9	SLYNTVATA
F111.27	9	SLYNAIATL
F111.28	9	SLYNLVAVL
F111.29	9	SLFNLLAVL
F111.32	9	SLFNTVVTL
F111.34	9	SLYNTVAAL
1039.031	9	MMWYWGPRL
1211.40	10	SLLNATAIAV
	10	TIHDIILECV
	9	FAFRDLCIV
	9	GTLGIVCPI
	9	TLGIVCPIC

Table 13

A	SEQUENCE	SOURCE
5	A	
	9 IPQSLDSWW	HBV ENV 191
	9 IPIPSSWAF	HBV ENV 313
	9 TPARVTGGV	HBV POL 365
	9 LPIFFCLWV	HBV ENV 379
	9 HPAAMPHLL	HBV POL 440
10	9 FPHCLAFSY	HBV POL 541
	9 DPSRGRLGL	HBV POL 789
	9 QPRGRRQPI	HCV Core 57
	9 SPRGSRPSW	HCV Core 99
	9 DPRRRSRNL	HCV Core 111
15	9 LPGCSFSIF	HCV Core 168
	9 YPCTVNFTI	HCV E2 622
	9 LPALSTGLI	HCV E2 681
	9 HPNIEEVAL	HCV NS3 1358
	9 SPGALVVGV	HCV NS4 1887

A	SEQUENCE	SOURCE
A		
9	SPGQRVEFL	HCV NS5 2615
9	APTLWARMI	HCV NS5 2835
9	FPRIWLHJL	HIV VPR 34
9	SPTRRELQV	HIV POL 37
9	FPVRPQVPL	HIV NEF 84
9	RPQVPLRPM	HIV NEF 87
9	KPCVKLTPL	HIV ENV 123
9	SPRTLNAWV	HIV GAG 153
9	FPISPIETV	HIV POL 171
9	SPAIFQSSM	HIV POL 327
9	NPDIVIYQY	HIV POL 346
9	GPGHKARVL	HIV GAG 360
9	LPEKDSWTV	HIV POL 417
9	YPLASLRSL	HIV GAG 507
15	VPRRKAKII	HIV POL 991
9	TPTLHEYML	HPV16 E7 5
9	KPLNPAEKL	HPV18 E6 110
9	NPAEKLRLH	HPV18 E6 113
9	VPISHLYIL	MAGE2 170
20	MPKTGLLII	MAGE2 196

A A	SEQUENCE	SOURCE
9	DPACYEFLW	MAGE2 265
9	EPHISYPPL	MAGE2 296
9	YPPLHERAL	MAGE2 301
9	LPTTMNYPL	MAGE3 71
9	DPIGHLYIF	MAGE3 170
9	MPKAGLLII	MAGE3 196
9	GPHISYPPL	MAGE3 296
9	HPSDGKCNL	P. falciparum S
9	RPRGDNFAV	P. falciparum S
10	QPRPRGDNF	P. falciparum S
9	LPNDKSDRY	P. falciparum S
10	LPLDKGIKPY	HBV POL 123
10	TPARVTGGVF	HBV POL 365
10	FPHCLAFSYM	HBV POL 541
15	LP RRGPRLGV	HCV Core 37
10	APLGGAAARAL	HCV Core 142
10	LPGCSFSIFL	HCV Core 168
10	VPASQVCGPV	HCV E2 497
10	YPCTVNFTIF	HCV E2 622

A A	SEQUENCE	SOURCE
10	SPLLLSTTEW	HCV E2 663
10	RPSGMFDSSV	HCV NS3 1506
10	LPVCQDHLEF	HCV NS3 1547
10	KPTLHGPTPL	HCV NS3 1614
5	TPLLYRLGAV	HCV NS3 1621
10	NPAIASLMAF	HCV NS4 1783
10	LPAILSPGAL	HCV NS4 1882
10	SPGALVVGVV	HCV NS4 1887
10	APTLWARMIL	HCV NS5 2835
10	IPVGEIYKRW	HIV GAG 261
10	YPLASLRSLF	HIV GAG 507
10	APTKAKRRVV	HIV ENV 547
10	VPISHLYILV	MAGE2 170
10	MPKTGLLIIV	MAGE2 196
15	HPRKLLMQDL	MAGE2 241
10	LPTTMNYPLW	MAGE3 71
10	MPKAGLLIIV	MAGE3 196

A A	SEQUENCE	SOURCE
10	IPYSPLSPKV	P. falciparum S
10	TPYAGEPAPF	P. falciparum S
9	FPDHQLDPA	HBV ENV 14
9	YPALMPLYA	HBV POL 640
9	LPVCAFSSA	HBV X 58
9	APLGGAAARA	HCV 142
9	DPTTPLARA	HCV 2806
9	FPYLVAYQA	HCV 1582
9	LPAILSPGA	HCV 1882
10	NPAIASLMA	HCV 1783
9	TPIDTTIMA	HCV 2551
9	TPLLYRLGA	HCV 1621
9	WPLLLLLLA	HCV 793
9	NPYNTPVFA	HIV POL 225
15	APLLLARA	PAP 4
9	HPQWVLTAA	PSA 52
10	IPIPSSWAFA	HBV ENV 313
10	TPPAYRPPNA	HBV NUC 128
10	APFTQCGYPA	HBV POL 633
20	LPIHTAELLA	HBV POL 712
10	GPCALRFTSA	HBV X 67

A	SEQUENCE	SOURCE
5	10 DPTTPLARAA	HCV 2806
	10 IPQAVVDMVA	HCV 339
	10 LPCSFTTLPA	HCV 674
	10 QPEKGGRKPA	HCV 2567
	10 VPHPNIEEVA	HCV 1356
	10 IPAETGQETA	HIV POL 820
	10 LPQGWKGSPA	HIV POL 320
	10 FPDLESEFQA	MAGE2/3 98
	10 DPIGHLYIFA	MAGE3 170
	9 EPLSLYAH1	HPV 6b/11 E1 2
10	9 PPLLVTSNI	HPV 6b/11 E1 5
	9 SPRLDAIKL	HPV 6b/11 E1 1
	9 TPKKNCIAI	HPV 6b/11 E1 4
	9 FPFDRNGNA	HPV 6b/11 E1 5
	10 CPPLLVTSNI	HPV 6b/11 E1 5
15	10 FPFDRNGNAV	HPV 6b/11 E1 5
	8 GPLVLQAA	HBV ENV 173
	8 IPIPSSWA	HBV ENV 313

A A	SEQUENCE	SOURCE
8	VPFVQWFV	HBV ENV 340
8	LPIFFCLW	HBV ENV 379
8	RPPNAPIL	HBV NUC 133
8	MPLSYQHF	HBV POL 1
8	HPAAMPHL	HBV POL 429
8	SPFLLAQF	HBV POL 511
8	YPALMPLY	HBV POL 640
8	SPTYKAFL	HBV POL 659
8	VPSALNPA	HBV POL 769
10	HPvhAGPI	HIV con. GAG
8	GPGvRyPL	HIV con. NEF
8	SPIETVPV	HIV con. POL
8	NPYNTPVF	HIV con. POL
8	LPIQKETW	HIV con. POL

A A	SEQUENCE	SOURCE
8	VPRRKaKj	HIV con. POL
8	VpLQLPPI	HIV con. REV
8	VPLAMKLI	P. falciparum
8	LPYGRNL	P. falciparum
8	RPRGDNFA	P. falciparum
8	IPQQEPNI	P. falciparum
8	TPFAGEPA	P. falciparum
9	SPINTIAEA	HPV 6b E1 93
9	SPISNVANA	HPV 11 E1 93
9	SPRLDAIKL	HPV 6b/11 E1 1
9	EPLSLYAH	HPV 6b/11 E1 2
9	EPPKIQSGV	HPV 6b/11 E1 3
9	IPFLTKFKL	HPV 6b E1 455
9	TPKKNCIAI	HPV 6b/11 E1 4
9	QPLTDAKVA	HPV 11 E1 512
9	PPLLVTSNI	HPV 6b/11 E1 5

A A	SEQUENCE	SOURCE
9	FPPFDRNGNA	HPV 6b/11 E1 5
9	APLILSRIV	PSA 14
9	HPEDTGQVF	PSA 78
9	HPLYDMSLL	PSA 94
5	HPQKVTKFM	PSA 184
9	GPLVCNGVL	PSA 211
9	RPSLYTKVV	PSA 235
9	FPPEGVSIW	PAP 124
9	NPILLWQPI	PAP 133
10	LPFRNCPRF	PAP 156
9	IPSYKKLIM	PAP 277
9	LPPYASCHL	PAP 307
9	SPSCPLERF	PAP 348
9	CPLERFAEL	PAP 351
15	GPTLIGANA	gp100 74
9	LPDGQVIWV	gp100 97
9	VPLAHSSSA	gp100 198
9	QPLTFALQL	gp100 236
9	DPSGYLAEA	gp100 246
20	EPGPVTAQV	gp100 282
9	MPTAESTGM	gp100 366
9	TPAEVSIVV	gp100 401
9	LPKEACMEI	gp100 520
25	LPSPACQLV	gp100 545
9	VPLIVGILL	gp100 596
9	LPHSSSHWL	gp100 630

A A	SEQUENCE	SOURCE
9	CPIGENSPL	gp100 647
9	SPLLSGQQV	gp100 653
9	MPREDAHFI	MART1 1
9	APLGPQFPF	Tyrosinase 6
9	IPIGTYGQM	Tyrosinase 1
9	TPMFNDINI	Tyrosinase 1
9	LPWHLRLFLL	Tyrosinase 2
9	IPYWDWRDA	Tyrosinase 2
9	SPASFFSSW	Tyrosinase 2
9	LPSSADVEF	Tyrosinase 3
9	SPLTGIADA	Tyrosinase 3
9	DPIFLLHHA	Tyrosinase 3
9	IPLYRNGDF	Tyrosinase 4
9	YPELPKPSI	CEA 141
9	LPVSPRLQL	CEA 185
9	LPVSPRLQL	CEA 363
9	NPPAQYSWL	CEA 442
9	LPVSPRLQL	CEA 541
9	IPQQHTQVL	CEA 632
9	NPPAQYSWF	CEA 264
9	LPSIPVHPI	Prost.Ca PSM
9	IPVHPIGYY	Prost.Ca PSM
9	RPFYRHVIY	Prost.Ca PSM
9	TPKHNMKAF	Prost.Ca PSM
9	FPGIYDALF	Prost.Ca PSM
9	RPRWLCAGA	Prost.Ca PSM
9	DPLTPGYPA	Prost.Ca PSM

A A	SEQUENCE	SOURCE
9	RPRRTILFA	Prost.Ca PSM
9	LPFDCRDYA	Prost.Ca PSM
9	LPIHTAELL	HBV POL 712
10	GPDAPTISPL	CEA 236
10	IPQQHTQVLF	CEA 632
10	QPIPVHTVPL	Prost.Ca PAP
10	HPYKDFIATL	Prost.Ca PAP
10	LPGCSPSCPL	Prost.Ca PAP
10	LPSWATEDTM	Prost.Ca PAP
10	VPLSEDQLLY	Prost.Ca PAP
10	FPHPLYDMSL	Prost.Ca PSA
10	RPGDDSSHDL	Prost.Ca PSA
10	HPQKVTKFML	Prost.Ca PSA
10	LPFDCRDYAV	Prost.Ca PSM
10	YPNKTHPNYI	Prost.Ca PSM
10	SPEFSGMPRI	Prost.Ca PSM
10	RPRWLCAGAL	Prost.Ca PSM
10	TPKHNMK AFL	Prost.Ca PSM
10	RPFYRHVIYA	Prost.Ca PSM
20	HPAAMPHLLV	HBV POL 429
9	SPREGPLPA	HER2/neu 1151
9	KPDLSYMPI	HER2/neu 605
9	HPPAFSPA	HER2/neu 1208

A A	SEQUENCE	SOURCE
9	GPLPAARPA	HER2/neu 1155
9	APQPHPPPA	HER2/neu 1204
9	EPLTPSGAM	HER2/neu 698
9	LPTHDPSP	HER2/neu 1101
5	DPLNNNTTPV	HER2/neu 121
9	SPLTSIISA	HER2/neu 649
9	SPKANKEIL	HER2/neu 760
9	LPTNASLSF	HER2/neu 65
9	CPSGVKPDL	HER2/neu 600
10	SPLAPSEGA	HER2/neu 1073
9	MPNQAQMRI	HER2/neu 706
9	LPAARPAGA	HER2/neu 1157
9	LPQPPICTI	HER2/neu 941
9	SPAFDNLYY	HER2/neu 1214

A A	SEQUENCE	SOURCE
9	TPTAENPEY	HER2/neu 1240
9	LPSETDGYV	HER2/neu 1120
10	LPTNASLSFL	HER2/neu 65
10	CPAEQRASPL	HER2/neu 642
10	KPCARVCYGL	HER2/neu 336
10	APQPHPPPAF	HER2/neu 1204
10	SPGGLRELQL	HER2/neu 133
10	SPLTSIISAV	HER2/neu 649
10	MPNQAQMRIL	HER2/neu 706
10	SPYVSRLLLGI	HER2/neu 779
10	HPPPAFSPAFA	HER2/neu 1208
10	SPREGPLPAA	HER2/neu 1151
10	NPHQALLHTA	HER2/neu 488
10	MPYGCLLDHV	HER2/neu 801

A	SEQUENCE	SOURCE
5	10 GPASPLDSTF	HER2/neu 995
	9 LPTTLFQPV	HTLV-I tax 21
	9 IPPSFLQAM	HTLV-I tax 10
	9 FPGFGQSLL	HTLV-I tax 4
	9 WPLLPHVIF	HTLV-I tax 16
	9 SPPITWPLL	HTLV-I tax 16
	9 VPYKRIEEL	HTLV-I tax 18
	9 RPQNLTYTLW	HTLV-I tax 13
	9 CPKDGQPSL	HTLV-I tax 26
	9 RPNDEVTAV	GCDFP-15 47
10	9 SPATLLLVL	GCDFP-15 11
	9 WPYLNRLV	HPV16 E1 576
	9 QPFILYAH	HPV18 E1 263
	9 SPRLKAICI	HPV16 E1 107

A	SEQUENCE	SOURCE
A		
9	SPLGERLEV	HPV18 E1 97
9	SPRLQEISL	HPV18 E1 110
9	RPIVQFLRY	HPV18 E1 447
10	WPYLHNRLVV	HPV16 E1 576
5	WPYLESRITV	HPV18 E1 583
10	QPPKLRSSVA	HPV18 E1 315
10	EPPKLRSTAA	HPV16 E1 308
9	DPSRGRLGL	HBV POL 778
9	HPAAMPHLL	HBV POL 429
10	IPIPSSWAF	HBV ENV 313
10	TPARVTGGVF	HBV POL 354
10	FPHCLAFSYM	HBV POL 530
9	LPVCAFSSA	HBV X 58
9	YPALMPLYA	HBV POL 640
15	APLLLARAA	PAP 4

5

10

A	SEQUENCE	SOURCE
9	HPQWVLTAA	PSA 52
9	HPSDGKCNL	Pf SSP2 206
9	RPRGDNFAV	Pf SSP2 305
9	QPRPRGDNF	Pf SSP2 303
10	TPYAGEPAPP	Pf SSP2 539
9	GPHISYPPL	MAGE3 296
9	YPPLHERAL	MAGE2 301
9	VPISHLYIL	MAGE2 170
9	EPHISYPPL	MAGE2 296
9	LPTTMNYPL	MAGE3 71
9	MPKAGLLII	MAGE3 196
10	HPRKLLMQDL	MAGE2 241

Table 14

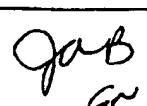
PEPTIDE	AA	SEQUENCE
25.0129	9	LPPLERLTL
26.0445	10	EPGPVTAQVV
26.0448	10	LPRIFCSCPPI
26.0449	10	LPSPACQLVL
26.0455	10	VPLAHSSSAF
26.0458	10	VPRNQDWLGV
26.0476	10	APPAYEKLSA
26.0478	10	MPREDAHFIY
26.0519	10	APAFLPWHRL
26.0522	10	GPNCTERRLL
26.0523	10	IPLYRNGDFF
26.0529	10	TPRLPSSADV
19.0101	9	TPAEVSIVV
26.0554	11	APFTQCGYPAL
26.0561	11	NPADDPSRGRL
26.0564	11	RPPNAPILSTL
26.0566	11	SPFLLAQFTSA
26.0567	11	SPHHTALRQAI
26.0568	11	TPARVTGGVFL

WHAT IS CLAIMED IS:

1. A composition comprising an immunogenic peptide having an HLA binding motif, which immunogenic peptide is a peptide shown in Tables 3-14 or a peptide comprising a conservative substitution of a residue in a peptide shown in Table 3-14.
- 5
2. The composition of claim 1, wherein the immunogenic peptide is linked to a second oligopeptide.
- 10
3. The composition of claim 2, wherein the second oligopeptide is a peptide that induces a helper T response.
- 15
4. A composition comprising a nucleic acid molecule encoding an immunogenic peptide as shown in Tables 3-14, or a peptide comprising a conservative substitution of a residue of a peptide shown in Table 3-14.
- 5
5. The composition of claim 4, wherein the nucleic acid further comprises a sequence encoding a second immunogenic peptide.
- 20
6. The composition of claim 4, wherein the nucleic acid further comprises a sequence encoding an oligopeptide that induces a helper T response.
- 25
7. A method of inducing a cytotoxic T cell response comprising contacting a cytotoxic T cell with a peptide of claim 1.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/05039

A. CLASSIFICATION OF SUBJECT MATTER IPC(6) : A61K 39/00, 39/29; C07K 7/00, 14/02, 14/82 US CL : 424/185.1; 530/300, 328, 350 According to International Patent Classification (IPC) or to both national classification and IPC													
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S. : 424/185.1; 530/300, 328, 350													
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched STN file=reg of first sequence in Table 3. Examiner's MHC/peptide files.													
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) STN file=reg sequence search of first sequence in Table 3. STN file=ca of hits on sequence search.													
C. DOCUMENTS CONSIDERED TO BE RELEVANT <table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="text-align: left; padding: 2px;">Category^a</th> <th style="text-align: left; padding: 2px;">Citation of document, with indication, where appropriate, of the relevant passages</th> <th style="text-align: left; padding: 2px;">Relevant to claim No.</th> </tr> </thead> <tbody> <tr> <td style="text-align: center; padding: 2px;">T</td> <td style="padding: 2px;">BRUSS, V. A short linear sequence in the pre-S domain of the large hepatitis B virus envelope protein required from virion formation. J. Virology. December 1997, Vol. 71, No. 12, pages 9350-9357. See entire document</td> <td style="text-align: center; padding: 2px;">1-3 and 7</td> </tr> <tr> <td style="text-align: center; padding: 2px;">Y</td> <td style="padding: 2px;">PREISLER-ADAMS, S. et al. Complete nucleotide sequence of a hepatitis B virus, subtype adw2, and identification of three types of C open reading frame. Nucleic Acids Res. 1993, Vol. 21, No. 9, page 2258. See entire document.</td> <td style="text-align: center; padding: 2px;">1-3 and 7</td> </tr> <tr> <td style="text-align: center; padding: 2px;">Y</td> <td style="padding: 2px;">RAMMENSEE, H. et al. Peptides naturally presented by MHC Class I molecules. Annu. Rev. Immunol. 1993, Vol. 11, pages 213-243, see entire article.</td> <td style="text-align: center; padding: 2px;">1-3 and 7</td> </tr> </tbody> </table>		Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.	T	BRUSS, V. A short linear sequence in the pre-S domain of the large hepatitis B virus envelope protein required from virion formation. J. Virology. December 1997, Vol. 71, No. 12, pages 9350-9357. See entire document	1-3 and 7	Y	PREISLER-ADAMS, S. et al. Complete nucleotide sequence of a hepatitis B virus, subtype adw2, and identification of three types of C open reading frame. Nucleic Acids Res. 1993, Vol. 21, No. 9, page 2258. See entire document.	1-3 and 7	Y	RAMMENSEE, H. et al. Peptides naturally presented by MHC Class I molecules. Annu. Rev. Immunol. 1993, Vol. 11, pages 213-243, see entire article.	1-3 and 7
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<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See parent family annex.													
<table border="0" style="width: 100%; border-collapse: collapse;"> <tr> <td style="width: 30%; vertical-align: top; padding: 2px;"> • Special categories of cited documents: •A• document defining the general state of the art which is not considered to be of particular relevance •B• earlier document published on or after the international filing date •L• document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reasons (as specified) •O• document referring to an oral disclosure, use, exhibition or other means •P• document published prior to the international filing date but later than the priority date claimed </td> <td style="width: 10%; vertical-align: top; padding: 2px;"> "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention </td> <td style="width: 10%; vertical-align: top; padding: 2px;"> "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone </td> <td style="width: 10%; vertical-align: top; padding: 2px;"> "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art </td> <td style="width: 10%; vertical-align: top; padding: 2px;"> "A" document member of the same patent family </td> </tr> </table>		• Special categories of cited documents: •A• document defining the general state of the art which is not considered to be of particular relevance •B• earlier document published on or after the international filing date •L• document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reasons (as specified) •O• document referring to an oral disclosure, use, exhibition or other means •P• document published prior to the international filing date but later than the priority date claimed	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	"A" document member of the same patent family							
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Date of the actual completion of the international search 12 MAY 1998	Date of mailing of the international search report 17 JUL 1998												
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230		Authorized officer THOMAS CUNNINGHAM  Telephone No. (703) 308-0196											

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/05039

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

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Y	ENGELHARD, V. et al. Structure of peptides associated with MHC Class I molecules. <i>Curr. Opin. Immunol.</i> 1994, Vol. 6, pages 13-23, see entire document.	1-3 and 7

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/05039

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
2. Claims Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See attached sheet.

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-3 and 7

Remark on Protest

The additional search fees were accompanied by the applicant's protest.
 No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/05039

Observations where unity of invention is lacking (Continuation of item 2 of first sheet)
1. This International Search Authority has found 3453 inventions claimed in the International Application covered by the claims indicated below:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s) 1-3 and 7, drawn to compositions comprising peptides and methods of inducing CTL responses using such compositions. A review of Tables 3-14 indicates there are 2764 structurally different peptides recited.

Group II, claim(s) 4-6, drawn to nucleic acids encoding peptides. Claims 4-6 recite nucleic acids encoding the 2764 different peptides of Tables 3-14.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. The species are as follows:

Each of the 2764 different peptides recited by Tables 3-14 and each of the 2764 different nucleic acid sequences encoding the peptides of Tables 3-14. $2764 + 2764 = 5,528$ total species.

The claims are deemed to correspond to the species listed above in the following manner:

The following claims are generic: claims 1-7 because they encompass all of the peptides or nucleic acid sequences encoding the peptides of Tables 3-14.

The first peptide species recited in Table 3 (FTF...LSK) will be examined. Each additional peptide species requires the payment of a separate fee. To have all the recited peptide species searched requires the payment of 2763 additional fees.

Upon payment for Group II, the Office will examine the first ten (or ten that the Applicant selects) nucleic acid species at no additional cost. Each four species of nucleic acids thereafter requires the payment of a separate fee. To have all the nucleic acid species searched requires the payment of $(2764-10)/4 = 689$ additional fees.

and it considers that the International Application does not comply with the requirements of unity of invention (Rules 13.1, 13.2 and 13.3) for the reasons indicated below:

The inventions listed as Groups I and II do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: the peptides of Group I lack the corresponding technical structural and functional features of the nucleic acids of Group II.

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons: the 5528 different species of peptides recited by Tables 3-14 (or the nucleic acid sequences encoding such peptides) lack the same or corresponding special technical features of common structure and function, source of isolation and amino acid or nucleic acid identity. Each separate species would require a separate prior art search.